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us-09-693-205a-47.may20.rge

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 22:17:57 ; Search time 1535 Seconds

(without alignments)
564,730 Million cell updates/sec

Title: US-09-693-205A-47

Perfect score: 20

Sequence: 1 gtgaatgccacttgcact 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 1036652

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb_hcg: *
3: gb_in: *
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6: gb_pat: *
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8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_srs: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *
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16: em_fun: *
17: em_hum: *
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28: em_un: *
29: em_vi: *
30: em_hcg_hum: *
31: em_hcg_inv: *
32: em_hcg_other: *
33: em_hcg_mus: *
34: em_hcg_dln: *
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41: em_hcgo_other: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13.2	66.0	24	6	AX290535
C 2	13	65.0	20	6	AR437040 Sequence
C 3	13	65.0	21	6	AX154399 Sequence
C 4	12.6	63.0	21	6	BD167262 Sequence
C 5	12.4	62.0	20	6	AR100612 Sequence
C 6	12.4	62.0	20	6	AR121611 Sequence
C 7	12.4	62.0	20	6	AR311314 Sequence
C 8	12.4	62.0	24	6	AX447358 Sequence
C 9	12.2	61.0	17	6	AR142556 Sequence
C 10	12.2	61.0	17	6	AR142558 Sequence
C 11	12.2	61.0	17	6	E49149
C 12	12.2	61.0	17	6	E49151
C 13	12	60.0	23	6	AX365154 Sequence
C 14	11.8	59.0	19	6	BD089690 Sequence
C 15	11.8	59.0	19	12	AB068455 Synthetic
C 16	11.8	59.0	21	6	AR212666 Sequence
C 17	11.6	58.0	19	6	AX082098 Sequence
C 18	11.6	58.0	19	6	AX082100 Sequence
C 19	11.6	58.0	20	6	AX316266 Sequence
C 20	11.6	58.0	24	6	BD179353 Insulin-1
C 21	11.6	58.0	24	6	BD179354 Insulin-1
C 22	11.6	58.0	24	9	HUMXP587B Homo sapien
C 23	11.6	58.0	25	6	AX609328 Sequence
C 24	11.4	57.0	17	6	BD254521 Regulator
C 25	11.4	57.0	17	6	AX758367 Sequence
C 26	11.4	57.0	19	6	BD266251 Universal
C 27	11.4	57.0	20	6	BD243093 Antisense
C 28	11.4	57.0	20	6	BD243094 Antisense
C 29	11.4	57.0	20	6	BD243095 Antisense
C 30	11.4	57.0	20	6	BD243096 Antisense
C 31	11.4	57.0	20	6	AX189426 Sequence
C 32	11.4	57.0	20	6	AX189430 Sequence
C 33	11.4	57.0	20	6	AX189430 Sequence
C 34	11.4	57.0	21	6	AR083899 Sequence
C 35	11.4	57.0	21	6	AR278835 Sequence
C 36	11.4	57.0	21	6	AX095410 Sequence
C 37	11.4	57.0	21	6	AX095574 Sequence
C 38	11.4	57.0	23	6	AR063162 Sequence
C 39	11.4	57.0	23	6	AR071358 Sequence
C 40	11.4	57.0	23	6	AR119344 Sequence
C 41	11.4	57.0	23	6	AX384685 Sequence
C 42	11.4	57.0	24	6	A63197 Sequence 11
C 43	11.4	57.0	24	6	AX443656 Sequence
C 44	11.4	57.0	25	6	AX447638 Sequence
C 45	11.2	56.0	17	6	AX579610 Sequence

ALIGNMENTS

RESULT 1
AX290535/c
LOCUS AX290535 24 bp DNA
DEFINITION Sequence 2297 from Patent WO0179548.
ACCESSION AX290535
VERSION AX290535.1 GI:17052218
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Baranyi,F., Zivvi,M., Gerry,N.P., Fawis,R. and Kilman,R.
AUTHORS Method of designing addressable array for detection of nucleic acid
TITLE sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 2297 25-OCT-2001;

CORNELL RESEARCH FOUNDATION, INC. (US)
 FEATURES
 Location/Qualifiers

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 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Hypothetical Probe Sequence"

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 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TGAATGGCCACTTGCAC 19
 DB 24 TGAGGCTCCACTTGCAC 7

RESULT 2
 LOCUS AR437040 20 bp DNA linear PAT 18-DEC-2003
 DEFINITION Sequence 92 from patent US 6656732.
 ACCESSION AR437040
 VERSION AR437040.1 GI:40200124
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Bennett,C.F. and Watt,A.T.
 TITLE Antisense inhibition of src-c expression
 JOURNAL Patent: US 6656732-A 92 02-DEC-2003;
 FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 65.0%; Score 13; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GGCCACTTGCAC 19
 DB 4 GGCCACTTGCAC 16

RESULT 3
 LOCUS AX154399 21 bp DNA linear PAT 22-JUN-2001
 DEFINITION Sequence 497 from Patent WO0138576.
 ACCESSION AX154399
 VERSION AX154399.1 GI:14536013
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
 TITLE Human single nucleotide polymorphisms
 JOURNAL Patent: WO 0138576-A 497 31-MAY-2001;
 WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
 FEATURES Location/Qualifiers
 source 1..21
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

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 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 TGAATGGCCACTTGG 16
 DB 7 TGATGGCCACTTGG 21

RESULT 4
 LOCUS BD167262 21 bp DNA linear PAT 17-JAN-2003
 DEFINITION Human liver disease-expressing genes.
 ACCESSION BD167262
 VERSION BD167262.1 GI:27873074
 KEYWORDS JP 2002209591-A/807.
 SOURCE unidentified
 ORGANISM unidentified
 Unclassified.

REFERENCE 1 (bases 1 to 21)
 AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
 TITLE Human liver disease-expressing genes
 JOURNAL Patent: JP 2002209591-A 807 30-JUL-2002;
 JAPAN SCIENCE AND TECHNOLOGY CORP
 OS Artificial Sequence
 PN JP 2002209591-A/807
 PD 30-JUL-2002
 PF 19-JAN-2001 JP 2001012328
 PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
 YAMASHITA
 PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
 PC C12P21/08,
 PC C12N15/00
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 CC Location/Qualifiers
 FT source 1..21
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FEATURES
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 /db_xref="taxon:32644"

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 Best Local Similarity 78.9%; Pred. No. 8.3e+04;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 TGAATGGCCACTTGCAC 20
 DB 19 TGATGACCACTTGCAC 1

RESULT 5
 LOCUS ARI00612/c 20 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 8 from patent US 6080727.
 ACCESSION ARI00612
 VERSION ARI00612.1 GI:12811060
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Zupl,G
 TITLE Oligonucleotide treatments and compositions for human melanoma
 JOURNAL Patent: US 6080727-A 8 27-JUN-2000;
 FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

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 Best Local Similarity 92.9%; Pred. No. 1.1e+05;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGCCACTTGGCACT 20
Db 16 GGCCACTTGGCACT 3

RESULT 6
LOCUS AR121611/c
DEFINITION Sequence 8 from patent US 6159946.
ACCESSION AR121611
VERSION AR121611.1 GI:14105187
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zaleski,A. and Shi,Y.
TITLE Antisense inhibition of c-myc to modulate the proliferation of smooth muscle cells
JOURNAL Patent: US 6159946-A 8 12-DEC-2000;
FEATURES
source Location/Qualifiers
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/organism="unknown"
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ORIGIN
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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGCCACTTGGCACT 20
Db 16 GGCCACTTGGCACT 3

RESULT 7
LOCUS AR311314
DEFINITION Sequence 1851 from patent US 6559294.
ACCESSION AR311314
VERSION AR311314.1 GI:31704740
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffiths,R., Holseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 1851 06-MAY-2003;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

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Best Local Similarity 92.9%; Pred.No.1.1e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGCCACTTGGCACT 20
Db 2 GGCCACTTGGCACT 15

RESULT 8
LOCUS AX447358/c
DEFINITION Sequence 3813 from Patent WO0216649.
ACCESSION AX447358
VERSION AX447358.1 GI:21696257
KEYWORDS

24 bp DNA linear PAT 05-JUL-2002

SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE
AUTHORS Gunderson,K.
TITLE Probes and decoder oligonucleotides
JOURNAL Patent: WO 0216649-A 3813 26-FEB-2002;
FEATURES
source Illumina, Inc. (US)
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."

ORIGIN
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Best Local Similarity 92.9%; Pred.No.1.1e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GAATGGCCACTTGG 16
Db 23 GAATGGCCACTTGG 10

RESULT 9
LOCUS AR142556
DEFINITION Sequence 15 from patent US 6203801.
ACCESSION AR142556
VERSION AR142556.1 GI:15103842
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Schaad,T.,Cornelis., Kuiper,C.Maria. and Vermeulen,A.Nicolaas.
TITLE Coccidioides polypeptide and vaccines
JOURNAL Patent: US 6203801-A 15 20-MAR-2001;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"

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Query Match 61.0%; Score 12.2; DB 6; Length 17;
Best Local Similarity 82.4%; Pred.No.1.4e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGATGGCCACTTGGC 17
Db 1 GTGATGGCCACTTGGC 17

RESULT 10
LOCUS AR142558
DEFINITION Sequence 17 from patent US 6203801.
ACCESSION AR142558
VERSION AR142558.1 GI:15103844
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Schaad,T.,Cornelis., Kuiper,C.Maria. and Vermeulen,A.Nicolaas.
TITLE Coccidioides polypeptide and vaccines
JOURNAL Patent: US 6203801-A 17 20-MAR-2001;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"

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Best Local Similarity 82.4%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGGCCACTTTGC 17
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1 GTGAATGGGAGCTTTC 17

Db 1 GTGAATGGGAGCTTTC 17

RESULT 11

E49149 17 bp DNA linear PAT 31-JAN-2002

LOCUS E49149
DEFINITION Coccidioides vaccine.
ACCESSION E49149
VERSION E49149.1 GI:18629274
KEYWORDS JP 2000219635-A/9.
SOURCE unclassified
ORGANISM unclassified

REFERENCE 1 (bases 1 to 17)
AUTHORS Schaepe,T.C., Kalberu,K.M. and Fuerumuren,A.N.
TITLE Coccidioides vaccine
JOURNAL Patent: JP 2000219635-A 9 08-AUG-2000;
AKZO NOBEL NV

COMMENT OS Unidentified
PN JP 2000219635-A/9
PD 08-AUG-2000
PE 01-OCT-1999 JP 1999281680
PR 07-OCT-1998 EP 98203384.7,16-OCT-1998 EP 98203457.1 PI
THODORUS CORNELISZ SCHAEPE,KATARINA MARIA KAIBERU, PI ALNOLDIUS
NICHOLAS FUERUMUREN

PC A61K39/00,A61K39/012,A61K39/108,A61K39/112,A61K39/15,A61K39/17, PC
A61K39/21,
PC A61K39/215,A61K39/235,A61K39/255,A61K39/39,A61P33/02, PC
C07K14/455,C12N15/09,
PC G01N33/569,C12N15/00
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CC Topology: Linear;
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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGGCCACTTTGC 17
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1 GTGAATGGGAGCTTTC 17

Db 1 GTGAATGGGAGCTTTC 17

RESULT 12

E49151 17 bp DNA linear PAT 31-JAN-2002

LOCUS E49151
DEFINITION Coccidioides vaccine.
ACCESSION E49151
VERSION E49151.1 GI:18629276
KEYWORDS JP 2000219635-A/11.
SOURCE unclassified
ORGANISM unclassified

REFERENCE 1 (bases 1 to 17)
AUTHORS Schaepe,T.C., Kalberu,K.M. and Fuerumuren,A.N.
TITLE Coccidioides vaccine
JOURNAL Patent: JP 2000219635-A 11 08-AUG-2000;
AKZO NOBEL NV

COMMENT OS AKZO NOBEL NV
PN Unidentified
PN JP 2000219635-A/11
PD 08-AUG-2000
PE 01-OCT-1999 JP 1999281680
PR 07-OCT-1998 EP 98203384.7,16-OCT-1998 EP 98203457.1 PI
THODORUS CORNELISZ SCHAEPE,KATARINA MARIA KAIBERU, PI ALNOLDIUS
NICHOLAS FUERUMUREN

PC A61K39/00,A61K39/012,A61K39/108,A61K39/112,A61K39/15,A61K39/17, PC
A61K39/21,
PC A61K39/215,A61K39/235,A61K39/255,A61K39/39,A61P33/02, PC
C07K14/455,C12N15/09,
PC G01N33/569,C12N15/00
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FEATURES
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ORIGIN

Query Match 61.0%; Score 12.2; DB 6; Length 17;
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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 1 GTGAATGGGAGCTTTC 17

RESULT 13

AX365154/c 23 bp DNA linear PAT 15-FEB-2002

LOCUS AX365154/c
DEFINITION Sequence 6 from Patent WO0200721.
ACCESSION AX365154
VERSION AX365154.1 GI:18696912
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
ARTIFICIAL SEQUENCES.

REFERENCE 1
AUTHORS Sprecher,C.A., Presnell,S.R., Gao,Z., Whitmore,T.E., Kuiper,J.L.
and Maurer,M.F.
TITLE Cytokine receptor zcytor17
JOURNAL Patent: WO 0200721-A 6 03-JAN-2002;
ZymoGenetics, Inc. (US)
Location/Qualifiers
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/mol_type='unassigned DNA'
/db_xref='taxon:32630'
/note='Oligonucleotide primer zc27698'

ORIGIN

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Best Local Similarity 75.0%; Pred. No. 1.8e+05;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTGAATGGCCACTTTGC 20
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22 GTGATGAGCTGCTGCGCT 3

Db 22 GTGATGAGCTGCTGCGCT 3

RESULT 14

BD089690/c 19 bp DNA linear PAT 27-AUG-2002

LOCUS BD089690/c
DEFINITION A method of arraying genome clone.
ACCESSION BD089690

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Page 5

VERSION BD089690.1 GI:22635300
KEYWORDS JP 2001321190-A/1934.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 19)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 1934 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKATSHA
COMMENT GENOTCHS
OS Artificial Sequence
PN JP 2001321190-A/1934
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00,
PC C12N15/00
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DB 16 TGGCCACTGAGCACT 2
RESULT 15
AB068455/c 19 bp DNA linear SYN 21-MAY-2003
LOCUS Synthetic construct DNA, reverse primer for human STS sts-cos26-T7
DEFINITION at 1p36.
ACCESSION AB068455
VERSION AB068455.1 GI:15129259
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
1
synthetic construct
synthetic construct
artificial sequences.
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source 1..19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
misc_feature 1..19

/note="reverse primer for human STS sts-cos26-T7 at 1p36
sts-cos26-T7 obtained from clones B307023, B191E13,
B191F10, B192B7, B192K5, B2806, B31F10, B382G16, B307020,
Human BAC library RPCI-11"
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Best Local Similarity 86.7%; Pred.No.2.3e+05;
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DB 16 TGGCCACTGAGCACT 2
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Job time : 1537 secs

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 22:14:37 ; Search time 331 seconds
(without alignments)
256.689 Million cell updates/sec

Title: US-09-693-205A-47
Perfect score: 20
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Scoring table: IDENTITY_NTC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124093041 residues

Total number of hits satisfying chosen parameters: 2488994

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseq1990s:*
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10: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	20	100.0	20	AAH20154	Aah20154 Human spa
2	14.2	71.0	25	ABL41475	Abi41475 Human DNA
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5	13	65.0	20	ABZ59471	Abz59471 Human src
6	12.8	64.0	21	AAC90263	Aac90263 Primer SN
7	12.8	64.0	21	ADD15186	Add15186 Reverse P
8	12.8	64.0	21	ACH54316	Ach54316 DNA target
9	12.6	63.0	21	ABV84997	Abv84997 Human gly
10	12.6	63.0	25	ACI25331	Ac125331 Human mtc
11	12.6	63.0	25	ACI94288	Ac194288 Human mtc
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14	12.4	62.0	20	AAQ70717	Aaq70717 C-myc gen
15	12.4	62.0	20	AAQ70717	Aaq70717 C-myc gen
16	12.4	62.0	20	AAQ70717	Aaq70717 C-myc gen
17	12.2	61.0	17	AAZ94912	Aaz94912 Elmeria t
18	12.2	61.0	18	AAZ94910	Aaz94910 Elmeria t
19	12.2	61.0	18	AAZ94910	Aaz94910 Elmeria t
20	12.2	61.0	23	AAZ94910	Aaz94910 Elmeria t
21	12.2	61.0	23	AAZ94910	Aaz94910 Elmeria t
22	12.2	61.0	23	AAZ94910	Aaz94910 Elmeria t
23	12.2	61.0	23	AAZ94910	Aaz94910 Elmeria t
24	12.2	61.0	23	AAZ94910	Aaz94910 Elmeria t
25	12.2	61.0	23	AAZ94910	Aaz94910 Elmeria t

C 24	12	60.0	25	8	ACI43788	Ac143788 Human mtc
C 25	11.8	59.0	15	4	AAFS2169	Aaf52169 IGF-I o11
C 26	11.8	59.0	19	6	ABL44890	Ab144890 Human chr
C 27	11.8	59.0	21	2	AAV84146	Aav84146 Human pro
C 28	11.8	59.0	21	4	AAFS987	Aaf95987 Human gen
C 29	11.8	59.0	21	4	AAH62596	Aah62596 CHRNA7 po
C 30	11.8	59.0	22	2	AAV00577	Aav00577 PCR prime
C 31	11.8	59.0	22	7	ADA05959	Ada05959 Human NOV
C 32	11.8	59.0	25	3	AAFS8093	Aac58093 Human PRO
C 33	11.8	59.0	25	8	ACH59115	Ach59115 DNA target
C 34	11.6	58.0	19	4	AAFS91257	Aaf91257 Human mul
C 35	11.6	58.0	19	4	AAFS91255	Aaf91255 Human mul
C 36	11.6	58.0	20	6	ABK24579	Abk24579 Human mul
C 37	11.6	58.0	21	9	ABK24579	Abk24579 Human mul
C 38	11.6	58.0	24	7	ABK21752	Abk21752 Human IGF
C 39	11.6	58.0	24	7	ABK21752	Abk21752 Human IGF
C 40	11.6	58.0	25	8	ACT76320	Act76320 Human mtc
C 41	11.6	58.0	25	8	ACT76321	Act76321 Human mtc
C 42	11.6	58.0	25	8	ACT80229	Act80229 Human mtc
C 43	11.6	58.0	25	8	ACT80229	Act80229 Human mtc
C 44	11.4	57.0	15	4	AAFS2168	Aaf52168 IGF-I o11
C 45	11.4	57.0	15	4	AAFS2167	Aaf52167 IGF-I o11

ALIGNMENTS

RESULT 1
AAH20154
ID AAH20154 standard; DNA; 20 BP.
XX
AC AAH20154;
XX
DT 09-AUG-2001 (first entry)
XX
DE Human spastin ORF PCR primer SEQ ID NO:47.
XX
KW Human; mouse; spastin; ARSACS; chromosome 13q11; identification;
KW autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation;
KW neurodegenerative disease; reduced sensory nerve conduction; diagnosis;
KW reduced motor nerve velocity; hypermyelination of retinal nerve fibre;
KW atrophy of upper cerebellar vermis; absence of Purkinje cell;
KW abnormal neuronal lipid storage; genetic disorder; characterisation;
KW PCR primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
OS
PN WO200129266-A2.
XX
PD 26-APR-2001.
XX
PF 20-OCT-2000; 2000WO-US029130.
XX
PR 20-OCT-1999; 99US-0160588P.
XX
PA (UWMC-) UNIV MCGILL.
PA (HOPI-) HOPITAL SAINTE-JUSTINE.
XX
HU Hudson TJ, Engert J, Richter A;
XX
WPI; 2001-308494/32.
XX
PT New isolated polymucleotide, encoding spastin gene, and polypeptides,
PT useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-
PT Saguenay disease by detecting two point mutations in spastin gene
PT sequence.
XX
PS Claim 23; Fig 7; 76pp; English.
XX
CC The present invention describes human and mouse spastin, and mutated
CC human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay
CC (ARSACS)) gene sequences (I). The spastin gene has been mapped to

CC chromosome 13q11. (I) have neuroprotective activities and can be used in
CC gene therapy and as a spastin polypeptide agonists. (I), their fragments
CC or their complements can be useful for assaying the presence of a nucleic
CC acid molecule in a sample. (I) is useful for diagnosing or aiding in the
CC diagnosis of an early onset neurodegenerative disease in an individual.
CC The neurodegenerative disease comprises reduced sensory nerve conduction,
CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres,
CC atrophy of upper cerebellar vermis, absence of Purkinje cells and
CC abnormal neuronal lipid storage. (I) can also be used to produce
CC antisense nucleic acids, is useful as molecular weight or chromosome
CC markers, to identify genetic disorders, as hybridisation probes or
CC primers, as an antigen, identify and express recombinant protein for
CC analysis, characterisation or therapeutic use, or as markers for tissues
CC in which the corresponding protein is expressed. Diagnostic methods from
CC the present invention can be used to identify subjects having or at risk
CC of developing a disease or disorder associated with aberrant expression
CC or activity of (I). The assays can be utilised to identify a subject
CC having or at risk of developing a disorder associated with Spastin
CC protein or spastin gene expression or activity. AAR20122 to AAR20173
CC represent specifically claimed primers which can be used in diagnostic
CC methods from the present invention

SO Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGATGGCCACTTTGGCACT 20
1 GTGATGGCCACTTTGGCACT 20
DB 1 GTGATGGCCACTTTGGCACT 20

RESULT 2
AB141475
ID AB141475 standard; DNA; 25 BP.

AC AB141475;

DT 27-AUG-2002 (first entry)

DE Human DNA-PK interaction protein 75 RT-PCR primer, SEQ ID NO:3.

Human DNA-PK interacting protein 75; KIP protein homologue;
recombinant production; malignant tumour; cancer; blood disease;
HIV infection; gene therapy; human immunodeficiency virus;
developmental disorder; immune disorder; inflammatory condition;
cytostatic; anti-inflammatory; immunomodulator; reverse transcription-PCR;
RT-PCR; primer; ss.

OS Homo sapiens.

PN CN1292385-A.

PD 25-APR-2001.

PF 10-OCT-1999; 99CN-00116950.

PR 10-OCT-1999; 99CN-00116950.

PA (SHAN-) SHANGHAI BODAO GENE TECHNOLOGY CO LTD.

PI Mao Y, Xie Y;

DR WPI; 2001-409811/44.

PT Polypeptide-human DNA-PK interaction protein 75 and polynucleotide coding
this polypeptide.

PS Example 3; Page 13 (Disclosure); 25pp; Chinese.

CC The invention relates to human DNA-PK interaction protein 75 (AB080943)
and nucleic acids encoding it (AB141474). The protein has a molecular

CC weight of 75 kD and has 34% identity and 62% homology over a 243 amino
CC acid stretch with a Caenorhabditis elegans KIP protein homologue shown in
CC Genbank accession number Z73098. The invention also relates to a method
CC for the recombinant production of the protein, an antagonist of the
CC protein, and the use of the protein, gene and antagonist in therapeutic
CC applications. DNA-PK interaction protein 75 can be used in the treatment
CC of a variety of diseases such as malignant tumours, blood diseases,
CC developmental disorders, HIV (human immunodeficiency virus) infection,
CC immune disorders and inflammatory conditions. Sequences AB141475-AB141476
CC represent reverse transcription-PCR (RT-PCR) primers used in an
CC exemplification of the invention to isolate human DNA-PK interaction
CC protein 75 cDNA

SO Sequence 25 BP; 7 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 71.0%; Score 14.2; DB 4; Length 25;
Best Local Similarity 84.2%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GTGATGGCCACTTTGGCAC 19
1 GTTATGGCCACTGTRCAC 19
DB 1 GTTATGGCCACTGTRCAC 19

RESULT 3
AB186991
ID AB186991 standard; DNA; 24 BP.

AC AB186991;

DT 15-FEB-2002 (first entry)

DE Capture oligonucleotide Zip ID#2297 oligo #2.

Human K-ras; PCR primer; probe; capture probe; mutation detection;
ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
oncogene; tumour suppressor; human papillomavirus; forensic;
environmental monitoring; food industry; feed industry; ss.

OS Synthetic.

PN WO200179548-A2.

PD 25-OCT-2001.

PF 04-APR-2001; 2001WO-US010958.

PR 14-APR-2000; 2000US-0197271P.

PA (CORR) CORNELL RES FOUND INC.

PI Barany F, Zilv M, Gerry NP, Favis R, Kliman R;

DR WPI; 2002-034366/04.

PT Designing capture oligonucleotide probes for use on a support to which
complementary oligonucleotides hybridize with little mismatch.

PS Example 5; Fig 25; 300pp; English.

The present invention describes a method (M1) for designing capture
oligonucleotide probes (I) for use on a support to which complementary
oligonucleotide probes (II) will hybridise with little mismatch, where
(I) have melting temperatures within a narrow range. The method is useful
for detecting infectious diseases caused by bacterial, infectious agents
e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
infectious agents e.g. Cryptococcus neoformans, Candida albicans and
Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
Epstein-Barr virus and polio virus, and parasitic infectious agents
selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
medinis. The method is also useful for detecting genetic diseases such
as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.

CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. AB182074 to
 CC AB197546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention

XX Sequence 24 BP, 5 A, 5 C, 9 G, 5 T, 0 U, 0 Other;

Query Match 66.0%; Score 13.2; DB 6; Length 24;
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGAATGCCACTTGCAC 19
 DB 1 TGAAGGTCACCTTGCAC 18

RESULT 4

AB186990/C
 ID AB186990 standard; DNA; 24 BP.

XX AB186990;

DT 15-FEB-2002 (first entry)

DE Capture oligonucleotide zip ID#2297 oligo #1.

XX Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KM ligation detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KM infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
 KM oncogene; tumour suppressor; human papillomavirus; forensic;
 KM environmental monitoring; food industry; feed industry; ss.

OS Synthetic.

PN WO200179548-A2.

PD 25-OCT-2001.

PF 04-APR-2001; 2001WO-US010958.

PR 14-APR-2000; 2000US-019271P.

XX (CORR) CORNELL RES FOUND INC.

PA Barany F, Zilvi M, Gerry NP, Favis R, Kilman R;

PI WPI, 2002-034366/04.

PT Designing capture oligonucleotide probes for use on a support to which
 PT complementary oligonucleotides hybridize with little mismatch.

XX Example 5; Fig 25; 300pp; English.

XX The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridize with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.

CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. AB182074 to
 CC AB197546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention

XX Sequence 24 BP, 5 A, 9 C, 5 G, 5 T, 0 U, 0 Other;

Query Match 66.0%; Score 13.2; DB 6; Length 24;
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGAATGCCACTTGCAC 19
 DB 24 TGAAGGTCACCTTGCAC 7

RESULT 5

AB259471
 ID AB259471 standard; DNA; 20 BP.

XX AB259471;

DT 17-APR-2003 (first entry)

DE Human src-c chimERIC phosphorothioate oligonucleotide SEQ ID NO:92.

XX Human; src-c; tyrosine kinase; src-c inhibitor; cytostatic; osteopathic;
 KM antiinflammatory; antibacterial; antisense therapy; vaccine; cancer;
 KM antisense oligonucleotide; aberrant bone remodeling; breast cancer;
 KM hyperproliferative disorder; pancreatic cancer; lung cancer; tumour;
 KM ovarian cancer; oesophageal cancer; neuroblastoma; retinoblastoma;
 KM Kaposi's sarcoma; infection; inflammation; tumour formation;
 KM phosphorothioate; ss.

OS Homo sapiens.

PD Synthetic.

PF Key Location/Qualifiers

FT modified_base 1..20

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PT New antisense oligonucleotides targeted to nucleic acids encoding src-c,
PT useful for diagnosing, treating or preventing diseases associated with
PT the expression of src-c, e.g. cancer or inflammation, and in research
PT applications.

PS Claim 3; Page 90; 137pp; English.

XX The present invention describes a compound (I) that is 8-50 nucleobases
CC in length targeted to a nucleic acid molecule encoding a 5'UTR, 3'UTR,
CC coding region, intron region, exon region, stop codon, intron:exon
CC junction, exon:exon junction, or 5' mRNA variant of src-c, and which
CC specifically hybridizes with and inhibits the expression of src-c. (I)
CC have cytoskeletal, antiinflammatory, osteopathic and antibacterial
CC activities, and can be used in antisense therapy and in vaccines. The
CC antisense compounds (I) can be used for modulating the expression of src-
CC c and for treating diseases or conditions associated with expression of
CC src-c, e.g. aberrant bone remodeling or hyperproliferative disorders,
CC particularly cancer, such as breast cancer, pancreatic cancer, lung
CC cancer, ovarian cancer, esophageal cancer, neuroblastoma, retinoblastoma
CC or Kaposi's sarcoma. (I) are also useful for diagnostics, therapeutics,
CC prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
CC formation, as research reagents and kits, and in distinguishing between
CC functions of various members of a biological pathway. The present
CC sequence represents a human src-c antisense chimeric phosphorothioate
CC oligonucleotide, which is used in an example from the present invention
XX

SQ Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 65.0%; Score 13; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GGCCACTTTGCAC 19
DB 4 GGCCACTTTGCAC 16

RESULT 6
AAC90263
ID AAC90263 standard; DNA; 21 BP.

AC AAC90263;

DT 14-MAR-2001 (first entry)

DE Primer SNORF33h 41F used to detect human SNORF33.

KM SNORF33; inflammation; arthritis; neurological disorder; infection;
KW bone disease; respiratory disorder; asthma; cancer; cardiovascular; ss.

OS Homo sapiens.

PN WO200073449-A1.

PD 07-DEC-2000.

PF 26-MAY-2000; 2000WO-US014654.

PR 28-MAY-1999; 99US-00322257.

PR 06-OCT-1999; 99US-00413433.

PA (SYNA-) SYNAPTIC PHARM CORP.

PI Borowsky BE, Ogozalek KU, Jones KA;

DR WPI; 2001-025252/03.

PT Nucleic acid encoding a mammalian (human, rat and mouse) SNORF33 receptor
PT which is useful for designing drugs for treating conditions such as a
PT chronic and acute inflammation, arthritis, neurological disorders and
PT microbial infections.

PS Disclosure; Page 123; 227pp; English.

XX The present invention relates to a mammalian SNORF33 receptor. SNORF33
CC antagonists and agonists are used to treat abnormalities brought about by
CC increased or decreased activity of the mammalian SNORF33 receptor. The
CC receptor is useful as a tool for designing drugs for treating conditions
CC such as a chronic and acute inflammation, arthritis, neurological
CC disorders, microbial infections, bone diseases, respiratory disorders
CC such as asthma, cancers, cardiovascular disorders
XX

SQ Sequence 21 BP; 3 A; 6 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 4; Length 21;
Best Local Similarity 87.5%; Pred. No. 5.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 ATGGCCACTTTGCAC 20
DB 2 ATGGCCACTTTGCAC 17

RESULT 7
ADD15186
ID ADD15186 standard; DNA; 21 BP.

AC ADD15186;

DT 15-JAN-2004 (first entry)

DE Reverse PCR primer to amplify the human XIST gene.

KW human; ss; PCR; primer; XIST; mental disorder;

KW differential gene expression; psychosis; schizophrenia; mood disorder;

KW bipolar; major depression; neuroleptic; antidepressant; gene therapy.

OS Homo sapiens.

PN WO2003039490-A2.

PD 15-MAY-2003.

PF 12-NOV-2002; 2002WO-US036663.

PR 09-NOV-2001; 2001US-0339252P.

PA (UYTE-) UNIV OFFICE TECHNOLOGY LICENSING STANFORD.

PI Akil H, Bunney WB, Burke S, Choudary PV, Cox DR, Evans SJ,

PI Jones BG, Li J, Lopez JF, Myers RM, Thompson R, Vawter MP,

PI Watson SJ;

DR WPI; 2003-441464/41.

PT Determining a predisposition to mental disorders utilizing differential

PT gene expression, useful for diagnosing, and/or treating mood disorders or

PT psychosis, including bipolar and major depression disorders and

PT schizophrenia.

XX Example 1; Page 57; 85pp; English.

XX This invention relates to a novel method for determining a predisposition
CC to mental disorders by utilizing differential gene expression.
CC Specifically, it refers to the differential gene expression of brain
CC region specific nucleic acids that can be used to determine a prevalence
CC of mental disorders with a gender bias. Accordingly, it comprises
CC contacting a patient's biological sample with a reagent (e.g. antibody)
CC that selectively associates with a polynucleotide given in the
CC specification, and detecting the level of reagent that associates to
CC determine whether the subject has, or is predisposed for, a mental
CC disorder. As such, the present invention describes a method and
CC compositions that are useful for diagnosing, and/or treating mental
CC disorders, such as psychosis e.g. schizophrenia or a mood disorder
CC including bipolar and major depression disorders. These compositions have
CC neuroleptic and antidepressant activities and can be used to treat the

CC aforementioned conditions via gene therapy routes. This oligonucleotide
CC sequence is a PCR primer used to amplify the differentially expressed
CC human XIST gene of the invention.

XX Sequence 21 BP; 3 A; 6 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 9; Length 21;
Best Local Similarity 87.5%; Pred. No. 5.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ATGGCCACTTTGCACT 20
DB 2 ATGGCCACTGTGACT 17

RESULT 8
ACH54316
ID ACH54316 standard; DNA; 25 BP.

XX ACH54316;
XX
XX 16-OCT-2003 (first entry)

DE DNA target sequence #3452 useful in array for genetic analyses.

XX Gene expression analysis; array; hybridisation; genetic variation;
XX tag-labelled compound; gene family; in situ hybridisation;
XX library screening; Southern hybridisation; northern hybridisation;
XX dot-blot hybridisation; gene sequence; mutation detection;
XX target sequence; probe; PCR; primer; ss.

XX Unidentified.

XX US2003082596-A1.

XX 01-MAY-2003.

XX 08-AUG-2002; 2002US-00215112.

XX 08-AUG-2001; 2001US-0311040P.

XX (MITT/) MITTMANN M.

XX Miltmann M;

XX WPI; 2003-576608/54.

XX New probe array useful e.g. for monitoring gene expression levels, for
XX analyzing genetic variations, or for hybridizing tag-labeled compounds,
XX comprises multiple nucleic acid probes.

XX Claim 1; SEQ ID NO 3452; 9pp; English.

XX The present invention relates to nucleic acid sequences that are
XX complementary to particular genes, and can be used as probes for a
XX variety of analyses, such as gene expression analysis. Each probe
XX comprises 9 or more consecutive nucleotides from at least one of 14936
XX nucleotide sequences defined in the patent, or their perfect sense match,
XX sense mismatch, antisense match or antisense mismatch oligonucleotides.

XX The probes may be used in an array comprising at least 10 distinct
XX nucleic acid probes. The array is useful in monitoring gene expression
XX levels by hybridisation to a DNA library, in analysing genetic

XX variations, and in hybridising tag-labelled compounds. The probes are
XX useful for identifying family members of a gene. The probes are also

XX useful in situ hybridisations, in screening cDNA or genomic libraries
XX (or derived subclones) for additional clones containing segments of DNA

XX that have been previously isolated and sequenced, in Southern, northern,
XX or dot-blot hybridisation of genomic DNA to identify or detect the

XX sequence of any gene or detect specific mutations in any gene, and in
XX mapping the 5' termini of mRNA molecules by primer extensions. The

XX nucleic acid sequences of the invention are also useful as PCR primers.
XX The invention provides a large collection of nucleic acid sequences

XX complementary to particular genes with a wide range of analytical uses.

CC ACH50865-ACH65260 represent the target sequences of the invention. Note:
CC The sequence data for this patent was obtained in electronic format
CC directly from the USPTO web site at seqdata.uspto.gov/psipdsidentry.html

XX Sequence 25 BP; 4 A; 5 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 8; Length 25;
Best Local Similarity 87.5%; Pred. No. 5.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGAATGGCCACTTTGC 17
DB 1 TGAATGGCCACTTTTC 16

RESULT 9
ABV84997/C
ID ABV84997 standard; DNA; 21 BP.

XX ABV84997;
XX
XX 12-DEC-2002 (first entry)

DE Human glypican 3 sense RT-PCR primer, SEQ ID NO:807.

XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
XX CH; liver tissue, hepatocellular carcinoma; cancer; tumour; HCC;
XX expression pattern; differential expression; reverse transcription-PCR;
XX RT-PCR; primer; ss.

XX Homo sapiens.

XX JP2002209591-A.

XX 30-JUL-2002.

XX 19-JAN-2001; 2001JP-00012328.

XX 19-JAN-2001; 2001JP-00012328.

XX (KAGA-) KAGAKU GIYUTSU SHINKO JIGYODAN.

XX WPI; 2002-631294/68.

XX Human chronic hepatitis C tissue expression exasperating gene group
XX comprises 100 high-ranking genes.

XX Disclosure; Page 130; 139pp; Japanese.

XX The invention relates to SAGE (serial analysis of gene expression) tags
XX representing groups of genes which are differentially expressed in human
XX chronic hepatitis C (CH) liver tissue or hepatitis C-induced

XX hepatocellular carcinoma (HCC) compared with normal human liver tissue.
XX The SAGE tags of this invention consist of a sequence of 10 nucleotides

XX located downstream of the 5'-CATG-3' sequence motif lying nearest to the
XX polyA region of cDNAs derived from a variety of genes. These tags serve

XX to uniquely identify each transcript and can thus be used to analyse the
XX pattern of gene expression in particular cell types. The invention also

XX relates to proteins encoded by the genes expressed in chronic hepatitis C
XX liver tissue or HCC, antibodies against these proteins, and inhibitors of

XX hepatitis C liver tissue or HCC. Groups of genes overexpressed in chronic
XX hepatitis C liver tissue or HCC may be used for the diagnosis and

XX treatment of these diseases. Such genes, inhibitors of their expression
XX or activity, and antibodies against the gene products may be used in the

XX development of drugs to treat chronic hepatitis C and/or HCC. Sequences
XX ABV84991-ABV85010 represent reverse transcription-PCR primers used in the

XX SAGE protocol to determine gene expression patterns in chronic hepatitis
XX C liver tissue and hepatocellular carcinoma compared with normal liver

XX tissue

XX Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 63.0%; Score 12.6; DB 6; Length 21;
Best Local Similarity 78.9%; Pred. No. 7e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

2 TGAATGGCCACTTTGGACT 20
19 TGCATGACCACTTGCAGT 1
Db

RESULT 10
ACI25331/c
ID ACI25331 standard; DNA; 25 BP.

AC ACI25331;

DT 13-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 25322.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX genetic variation; diallelic marker; polymorphism; human;
KM cross-species comparison.

OS Homo sapiens.

PN US2003104410-A1.

PD 05-JUN-2003.

PF 15-MAR-2002; 2002US-00098263.

PR 16-MAR-2001; 2001US-0276759P.

PA (AFFY-) AFFYMETRIX INC.

PI Miltmann MP;

DR WPI; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

PS Claim 1; SEQ ID NO 25322; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labeled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying diallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 8 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 63.0%; Score 12.6; DB 8; Length 25;

Best Local Similarity 78.9%; Pred. No. 7.2e+03;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 GTGAATGGCCACTTTGCAC 19
19 GTTAAGCTCAGCTTGCAC 1
Db

RESULT 11
ACI94288/c
ID ACI94288 standard; DNA; 25 BP.

AC ACI94288;

DT 14-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 94279.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX genetic variation; diallelic marker; polymorphism; human;
KM cross-species comparison.

OS Homo sapiens.

PN US2003104410-A1.

PD 05-JUN-2003.

PF 15-MAR-2002; 2002US-00098263.

PR 16-MAR-2001; 2001US-0276759P.

PA (AFFY-) AFFYMETRIX INC.

PI Miltmann MP;

DR WPI; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

PS Claim 1; SEQ ID NO 94279; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labeled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying diallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 9 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 63.0%; Score 12.6; DB 8; Length 25;

Best Local Similarity 78.9%; Pred. No. 7.2e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TGAATGCCACTTTGCACT 20
 |||||
 DB 25 TGAACAGGCACTTTCACACT 7

RESULT 12

AAQ70717/c
 ID AAQ70717 standard; DNA; 20 BP.

AC AAQ70717;

DT 25-MAR-2003 (revised)

DT 22-FEB-1995 (first entry)

XX C-myc gene antisense oligo.

XX C-myc; oncogene; smooth muscle; antisense; phosphorothioate;
 KW oligonucleotide; restenosis; ss.

XX Synthetic.

XX WO9415646-A1.

XX 21-JUL-1994.

XX 07-JAN-1994; 94WO-US0000265.

XX 07-JAN-1993; 93US-00004799.

XX (UVE-) UNIV JEFFERSON THOMAS.

XX Zaleski A, Shi Y;

XX WPI; 1994-248909/30.

XX Use of antisense oligonucleotides specific for c-myc - for modulating the
 PT proliferation of smooth muscle cells, partic. for treating or preventing the
 PT restenosis.

XX Example 12; Page 29; 52pp; English.

XX An oligonucleotide (AAQ70710) antisense to a segment of human c-myc mRNA
 CC beginning with a translational initiation codon reduced neointima
 CC formation in the coronary vasculature in a pig restenosis model. Activity
 CC was compared to that of antisense oligos (AAQ70715-21) that targeted
 CC other regions of c-myc mRNA. The oligo given in AAQ70717 targeted
 CC nucleotides 365-384 of the 5' non-coding region and provided a lower
 CC degree of growth inhibition than the AAQ70710 oligo. (Updated on 25-MAR-
 CC 2003 to correct PN field.)

XX Sequence 20 BP; 4 A; 9 C; 5 G; 2 T; 0 U; 0 Other;

XX Query Match 62.0%; Score 12.4; DB 2; Length 20;

XX Best Local Similarity 92.9%; Pred. No. 8.8e+03;

XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGCCACTTTGCACT 20
 |||||
 DB 16 GGCGACTTTGCACT 3

RESULT 13

AA95341/c

ID AA95341 standard; DNA; 20 BP.

AC AA95341;

DT 20-APR-1998 (first entry)

XX Treatment of human melanoma using c-myc oligonucleotide 8.

XX Melanoma; c-myc oligonucleotide; c-myc mRNA; cis-platin; inhibition;
 KW metastasis; treatment; proliferation; human; tumour; ss.

XX Synthetic.
 OS Homo sapiens.

XX WO9736005-A1.

XX 02-OCT-1997.

XX 24-MAR-1997; 97WO-US004703.

XX 26-MAR-1996; 96US-0014089P.

XX (LYNX-) LYNX THERAPEUTICS INC.

XX Zuppi G;

XX WPI; 1997-489662/45.

XX Inhibiting proliferation of human melanoma cells with anti-c-myc
 PT oligonucleotide(s) - particularly used together with cis-platin,
 PT inhibits metastasis, induces regression or prevents further growth.

XX Claim 1; Page 22; 68pp; English.

XX This c-myc oligonucleotide is complementary to a sequence of human c-myc
 CC mRNA and is used for inhibiting the proliferation of human melanoma cells
 CC (HMC). The c-myc oligonucleotide is at least 10 bases long and inhibits
 CC proliferation of HMC by at least 10 percent at 10 mu M, when the cells
 CC are cultured at 37 degree. C in presence of serum. The method is
 CC particularly used to treat human melanoma, and inhibits metastasis,
 CC promotes regression or prevents any increase in tumour mass. The c-myc
 CC oligonucleotide can be used together with cis-platin and which then
 CC reduces resistance of tumour cells to cis-platin. The oncogene c-myc is
 CC found to be essential for growth and metastasis of melanoma, and the c-
 CC myc oligonucleotides are designed to target double-stranded DNA or single
 CC stranded RNA. A combination of c-myc oligonucleotide and cis-platin is
 CC more effective than either component used alone

XX Sequence 20 BP; 4 A; 9 C; 5 G; 2 T; 0 U; 0 Other;

XX Query Match 62.0%; Score 12.4; DB 2; Length 20;

XX Best Local Similarity 92.9%; Pred. No. 8.8e+03;

XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGCCACTTTGCACT 20
 |||||
 DB 16 GGCGACTTTGCACT 3

RESULT 14

AA92550

ID AA92550 standard; DNA; 20 BP.

AC AA92550;

DT 13-SEP-1999 (first entry)

XX PCR primer used to amplify an ORF of Chlamydia pneumoniae.

XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 KW neutralising epitope; PCR primer; ss.

XX Synthetic.

XX Chlamydia pneumoniae.

XX WO927105-A2.

XX 03-JUN-1999.

XX 20-NOV-1998; 98WO-IB001890.

XX 21-NOV-1997; 97FR-00014673.

PR 04-NOV-1998; 98US-0107078P.
 XX (GEST) GENSET.
 XX Griffais R;
 PI WPI; 1993-357842/30.
 DR XX
 XX Genome sequence of Chlamydia pneumoniae.
 PT
 PS Page 1520; Disclosure; 1912pp; English.
 XX
 CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
 CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
 CC (see AAX91990). C. pneumoniae causes respiratory disease such as
 CC pneumonia and bronchitis and is thought to be a contributing factor in
 CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AAY34584-AAY35879) can be used
 CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleotide sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae
 XX
 SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 2; Length 20;
 Best Local Similarity 92.9%; Pred. No. 8.8e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGGCAGCTTGCACT 20
 |||||
 DB 2 GGGCAGCTTGCGCT 15

RESULT 15
 ID AAS62210/C
 XX AAS62210 standard; DNA; 23 BP.
 AC AAS62210;
 XX
 XX 29-JAN-2002 (first entry)
 DT
 XX
 DE Porcine forward PCR primer for GAPDH.
 XX
 KM Pig; muscular steatosis-modulating factor; ss; metabolic; muscular; MSWF;
 KM food supplement; obesity; hyperlipidaemia; atherosclerosis;
 KM wound healing; tumour; amyotrophic lateral sclerosis; ALS; PCR primer.
 XX
 OS Sus scrofa.
 XX
 XX W0200179287-A2.
 PN
 PD 25-OCT-2001.
 XX
 XX 12-APR-2001; 2001WO-CA000509.
 PF
 XX 17-APR-2000; 2000US-0197936P.
 PR
 XX (MIG) CANADA AGRIC & AGRI-FOOD CANADA.
 PA
 XX PI Palin M, Pomar C, Garlepy C;
 XX
 DR WPI; 2002-017600/02.
 XX

Prognosis and diagnosis of muscular steatosis, useful e.g. for selecting
 PT animals for breeding, by measuring levels of specific markers, also
 PT treating or inducing steatosis.

Example 1; Page 41; 190pp; English.

XX The invention relates to prognosis or diagnosis of muscular steatosis by
 CC measuring the level of a muscular steatosis modulating factor (MSWF) in a

CC human or animal and comparing this with the level in a healthy control.
 CC Any difference indicates presence of, or predisposition to, muscular
 CC steatosis. The method is particularly used for diagnosis or prognosis of
 CC muscular steatosis in mammals and birds, e.g. to select individuals as
 CC founders in animal breeding. Also (ant)agonists of MSWF can be used to
 CC treat, or induce (for increasing the fat content of food) muscular
 CC steatosis, in humans and animals. The MSWF markers are also useful in the
 CC study of diseases and conditions such as obesity, hyperlipidaemia,
 CC atherosclerosis, wound healing, tumours and amyotrophic lateral sclerosis
 CC (ALS). The present sequence is a PCR primer used to amplify a MSWF of the
 CC invention from its gene
 XX

SQ Sequence 23 BP; 5 A; 6 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 6; Length 23;
 Best Local Similarity 92.9%; Pred. No. 9e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 AATGGCAGCTTGCC 17
 |||||
 DB 17 AATGGCAGCTTGCC 4

Search completed: May 27, 2004, 01:16:28
 Job time : 335 secs

Thu May 27 10:14:59 2004

us-09-693-205a-47.may20.rn1

Page 1

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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 00:50:52 ; Search time 80 Seconds
(without alignments)
138.738 Million cell updates/sec

Title: US-09-693-205A-47

Perfect score: 20

Sequence: 1 ggcacgttgac 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 519696

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A-COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B-COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A-COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B-COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCOTUS-COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfile01.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	65.0	20	4	US-09-860-473-92
2	12.4	62.0	20	3	US-08-827-036A-8
3	12.4	62.0	20	3	US-08-481-341-8
4	12.4	62.0	20	4	US-09-198-452A-1851
5	12.4	62.0	20	5	PCT-US94-00265-8
6	12.2	61.0	17	3	US-09-411-578-15
7	12.2	61.0	17	3	US-09-411-578-17
8	12.2	61.0	17	4	US-09-749-233-15
9	12.2	61.0	17	4	US-09-749-233-17
10	12.2	61.0	17	4	US-09-540-014-14
11	12	60.0	23	4	US-08-540-259-1
12	11.8	59.0	21	4	US-09-442-143A-29
13	11.4	57.0	20	3	US-09-323-743-54
14	11.4	57.0	20	3	US-09-323-743-55
15	11.4	57.0	20	3	US-09-323-743-56
16	11.4	57.0	20	3	US-09-323-743-57
17	11.4	57.0	21	2	US-08-665-202-129
18	11.4	57.0	21	4	US-08-847-844A-115
19	11.4	57.0	21	4	US-09-315-574-129
20	11.4	57.0	21	4	US-09-642-894A-7
21	11.4	57.0	23	2	US-08-359-705B-16
22	11.4	57.0	23	2	US-08-286-846A-16
23	11.4	57.0	23	2	US-08-457-880A-16
24	11.4	57.0	23	3	US-08-444-622A-16
25	11.4	57.0	23	3	US-08-942-562-16
26	11.4	57.0	23	3	US-09-156-923-16
27	11.4	57.0	24	4	US-08-759-436-10

28	11.2	56.0	18	3	US-09-205-143-68	Sequence 68, Appl
29	11.2	56.0	18	3	US-09-632-580A-20	Sequence 20, Appl
30	11.2	56.0	19	4	US-09-422-978-10969	Sequence 10969, A
31	11.2	56.0	20	3	US-09-487-445-82	Sequence 82, Appl
32	11.2	56.0	20	4	US-09-091-952A-98	Sequence 98, Appl
33	11.2	56.0	20	4	US-09-375-318-20	Sequence 20, Appl
34	11.2	56.0	21	1	US-08-308-949A-16	Sequence 16, Appl
35	11.2	56.0	21	1	US-09-079-812E-11	Sequence 11, Appl
36	11.2	56.0	22	4	US-09-823-543-28	Sequence 28, Appl
37	11.2	56.0	23	4	US-09-026-958-7	Sequence 7, Appl
38	11.2	56.0	23	4	US-09-390-207-35	Sequence 35, Appl
39	11.2	56.0	23	4	US-09-612-033B-2	Sequence 2, Appl
40	11.2	56.0	23	4	US-09-798-051-12	Sequence 12, Appl
41	11.2	56.0	25	3	US-09-176-666-29	Sequence 29, Appl
42	11	55.0	20	3	US-08-894-818B-40	Sequence 40, Appl
43	11	55.0	20	3	US-08-894-818B-41	Sequence 41, Appl
44	11	55.0	20	4	US-09-445-472-20	Sequence 20, Appl
45	11	55.0	20	4	US-09-445-472-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-860-473-92
Sequence 92, Application US/09860473
Patent No. 6656732
GENERAL INFORMATION:
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF SRC-C EXPRESSION
FILE REFERENCE: RFS-0222
CURRENT APPLICATION NUMBER: US/09/860,473
CURRENT FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 169
SEQ ID NO 92
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-860-473-92

Query Match 65.0%; Score 13; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+02; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;

QY 7 GGCACCTTGCAC 19
|||||||
DB 4 GGCACCTTGCAC 16

RESULT 2
US-08-827-036A-8/c
Sequence 8, Application US/08827036A
Patent No. 6080727
GENERAL INFORMATION:
APPLICANT: Gabriella Zupi
TITLE OF INVENTION: Oligonucleotide Treatments and
TITLE OF INVENTION: Compositions for Human Melanoma
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: James A. Bradburne, Ph.D.
STREET: 5 Palo Alto Square,
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0

SOFTWARE: Microsoft Word for Windows, vers. 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,036A
FILING DATE: 03/25/97
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 60/014,089
FILING DATE: 26-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: James A. Bradburne, Ph.D.
REGISTRATION NUMBER: 38,389
REFERENCE/DOCKET NUMBER: LYNX-031/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 843-5095
TELEFAX: (650) 857-0663
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 nucleotides
STRANDEDNESS: single
TOPOLOGY: linear
US-08-827-036A-8

Query Match 62.0%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 8.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGCCACTTGCCT 20
DB 16 GGCCACTTGCCT 3

RESULT 3
US-08-481-341-8/c
Sequence 8, Application US/08481341
Patent No. 6159946
GENERAL INFORMATION:
APPLICANT: Zalewski, Andrew and Shi, Yi
TITLE OF INVENTION: ANTISENSE INHIBITION OF
TITLE OF INVENTION: C-MYC TO MODULATE THE PROLIFERATION
TITLE OF INVENTION: OF SMOOTH MUSCLE CELLS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavoigna
ADDRESSEE: & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS/DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,341
FILING DATE: January 7, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,799
FILING DATE: January 7, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Daniel A. Monaco
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 831-9 C11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-481-341-8

Query Match 62.0%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 8.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGCCACTTGCCT 20
DB 16 GGCCACTTGCCT 3

RESULT 4
US-09-198-452A-1851
Sequence 1851, Application US/09198452A
Patent No. 6559284
GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragm
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, p
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1851
LENGTH: 20
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1851

Query Match 62.0%; Score 12.4; DB 4; Length 20;
Best Local Similarity 92.9%; Pred. No. 8.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGCCACTTGCCT 20
DB 2 GGCCACTTGCCT 15

RESULT 5
PCT-US94-00265-8/c
Sequence 8, Application PC/TUS9400265
GENERAL INFORMATION:
APPLICANT: Thomas Jefferson University
TITLE OF INVENTION: ANTISENSE INHIBITION OF
TITLE OF INVENTION: C-MYC TO MODULATE THE PROLIFERATION
TITLE OF INVENTION: OF SMOOTH MUSCLE CELLS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavoigna
ADDRESSEE: & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH 720 KB
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS/DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00265
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 004,799
FILING DATE: January 7, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Daniel A. Monaco

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REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
PCT-US94-00265-8

Query Match 62.0%; Score 12.4; DB 5; Length 20;
Best Local Similarity 92.9%; Pred. No. 8.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GGCCACTTGGCACT 20
DB 16 GGCACTTGGCACT 3

RESULT 6
US-09-411-578-15
Sequence 15, Application US/09411578
Patent No. 6203801
GENERAL INFORMATION:
APPLICANT: Schaad, Theodorius C
APPLICANT: Kuiper, Catharina M
APPLICANT: Vermeulen, Arnoldus N
TITLE OF INVENTION: Coccioidosis Vaccines
FILE REFERENCE: schaad
CURRENT APPLICATION NUMBER: US/09/411,578
CURRENT FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: 98203384.7
EARLIER FILING DATE: 1998-10-07
EARLIER APPLICATION NUMBER: 98203457.1
EARLIER FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 15
LENGTH: 17
TYPE: DNA
ORGANISM: Eimeria tenella
US-09-411-578-15

Query Match 61.0%; Score 12.2; DB 3; Length 17;
Best Local Similarity 82.4%; Pred. No. 1e+03; 3; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGGCACTTGC 17
DB 1 GTGAATGGCACTTGC 17

RESULT 7
US-09-411-578-17
Sequence 17, Application US/09411578
Patent No. 6203801
GENERAL INFORMATION:
APPLICANT: Schaad, Theodorius C
APPLICANT: Kuiper, Catharina M
APPLICANT: Vermeulen, Arnoldus N
TITLE OF INVENTION: Coccioidosis Vaccines
FILE REFERENCE: schaad
CURRENT APPLICATION NUMBER: US/09/411,578
CURRENT FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: 98203384.7
EARLIER FILING DATE: 1998-10-07
EARLIER APPLICATION NUMBER: 98203457.1
EARLIER FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 41

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 17
LENGTH: 17
TYPE: DNA
ORGANISM: Eimeria tenella
US-09-411-578-17

Query Match 61.0%; Score 12.2; DB 3; Length 17;
Best Local Similarity 82.4%; Pred. No. 1e+03; 3; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGGCACTTGC 17
DB 1 GTGAATGGCACTTGC 17

RESULT 8
US-09-749-233-15
Sequence 15, Application US/09749233
Patent No. 668061
GENERAL INFORMATION:
APPLICANT: Schaad, Theodorius C
APPLICANT: Kuiper, Catharina M
APPLICANT: Vermeulen, Arnoldus N
TITLE OF INVENTION: Coccioidosis Vaccines
FILE REFERENCE: schaad
CURRENT APPLICATION NUMBER: US/09/749,233
CURRENT FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 09/411,578
PRIOR FILING DATE: 1999-10-04
PRIOR APPLICATION NUMBER: 98203457.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 15
LENGTH: 17
TYPE: DNA
ORGANISM: Eimeria tenella
US-09-749-233-15

Query Match 61.0%; Score 12.2; DB 4; Length 17;
Best Local Similarity 82.4%; Pred. No. 1e+03; 3; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGAATGGCACTTGC 17
DB 1 GTGAATGGCACTTGC 17

RESULT 9
US-09-749-233-17
Sequence 17, Application US/09749233
Patent No. 668061
GENERAL INFORMATION:
APPLICANT: Schaad, Theodorius C
APPLICANT: Kuiper, Catharina M
APPLICANT: Vermeulen, Arnoldus N
TITLE OF INVENTION: Coccioidosis Vaccines
FILE REFERENCE: schaad
CURRENT APPLICATION NUMBER: US/09/749,233
CURRENT FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 09/411,578
PRIOR FILING DATE: 1999-10-04
PRIOR APPLICATION NUMBER: 98203457.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 17
LENGTH: 17
TYPE: DNA
ORGANISM: Eimeria tenella
US-09-749-233-17

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Page 4

Query Match 61.0%; Score 12.2; DB 4; Length 17;
Best Local Similarity 82.4%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGATGGCCACTTGC 17
Db 1 GTGATGGCCACTTGC 17

RESULT 10
US-09-540-014-14/c
Sequence 14, Application US/09540014
Patent No. 6380372
GENERAL INFORMATION:
APPLICANT: Cho, Myeong-Je
APPLICANT: Del Val, Greg
APPLICANT: Caillaud, Maxime
APPLICANT: Lemaux, Peggy G.
APPLICANT: Buchanan, Bob B.
TITLE OF INVENTION: Barley Gene for Thiodoxin and
TITLE OF INVENTION: NADP-Thiodoxin Reductase
FILE REFERENCE: 2001-0701.30
CURRENT APPLICATION NUMBER: US/09/540.014
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 60/127,198
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: US 60/169,162
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 60/177,740
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 60/177,739
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: degenerative primer
US-09-540-014-14

Query Match 61.0%; Score 12.2; DB 4; Length 23;
Best Local Similarity 57.9%; Pred. No. 1.1e+03;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGATGGCCACTTGC 19
Db 21 GTGATGGCCACTTGC 3

RESULT 11
US-08-540-259-1
Sequence 1, Application US/08540259
Patent No. 6013516
GENERAL INFORMATION:
APPLICANT: Verma, Indar
APPLICANT: Trono, Didier
APPLICANT: Naldini, Luigi
APPLICANT: Galley, Philippe
TITLE OF INVENTION: VECTOR AND METHOD OF USE FOR NUCLEIC
TITLE OF INVENTION: ACID DELIVERY TO NON-DIVIDING CELLS
FILE REFERENCE: 07251/002001
CURRENT APPLICATION NUMBER: US/08/540.259
CURRENT FILING DATE: 1995-10-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: oligonucleotide for PCR

US-08-540-259-1
Query Match 60.0%; Score 12; DB 3; Length 23;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTGATGGCCACTTGC 20
Db 1 GTGATGGCCACTTGC 20

RESULT 12
US-09-442-143A-29/c
Sequence 29, Application US/09442143A
Patent No. 6403089
GENERAL INFORMATION:
APPLICANT: Levy, Gary
APPLICANT: Clark, David A.
TITLE OF INVENTION: Methods of Modulating Immune Coagulation
FILE REFERENCE: 9579-14
CURRENT APPLICATION NUMBER: US/09/442.143A
CURRENT FILING DATE: 1999-11-15
PRIOR FILING DATE: 1997-05-17
PRIOR APPLICATION NUMBER: US 60/046,537
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: US 60/061,684
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-442-143A-29

Query Match 59.0%; Score 11.8; DB 4; Length 21;
Best Local Similarity 86.7%; Pred. No. 1.8e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GAATGGCCACTTGC 17
Db 19 GATTTGCCACTTGC 5

RESULT 13
US-09-323-743-54/c
Sequence 54, Application US/09323743
Patent No. 6214986
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Wonda, Brett P.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, Qingsong
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0368
CURRENT APPLICATION NUMBER: US/09/323.743
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 09/277,020
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 54
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-323-743-54

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Query Match 57.0%; Score 11.4; DB 3; Length 20;
Best Local Similarity 92.3%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 TGAATGGCCACTT 14
Db 13 TGGATGGCCACTT 1

RESULT 14
US-09-323-743-55/c
Sequence 55, Application US/09323743
Patent No. 6214986
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, QingQing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0368
CURRENT APPLICATION NUMBER: US/09/323,743
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 09/277,020
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 55
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-323-743-55

Query Match 57.0%; Score 11.4; DB 3; Length 20;
Best Local Similarity 92.3%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TGAATGGCCACTT 14
Db 15 TGGATGGCCACTT 3

RESULT 15
US-09-323-743-56/c
Sequence 56, Application US/09323743
Patent No. 6214986
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, QingQing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0368
CURRENT APPLICATION NUMBER: US/09/323,743
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 09/277,020
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 56
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-323-743-56

Query Match 57.0%; Score 11.4; DB 3; Length 20;
Best Local Similarity 92.3%; Pred. No. 2.9e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 TGAATGGCCACTT 14
Db 17 TGGATGGCCACTT 5

Search completed: May 27, 2004, 02:24:07
Job time : 81 secs

Thu May 27 10:15:00 2004

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Page 1

GenCore version 5.1.6
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CM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 01:42:23 ; Search time 312 Seconds
(without alignments)
291.329 Million cell updates/sec

Title: US-09-693-205a-47
Perfect score: 20
Sequence: 1 gtgaatggccacttgcact 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2953838 seqs, 2272363821 residues

Total number of hits satisfying chosen parameters: 1135042

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	13.2	66.0	20	17	US-10-210-479-119
3	12.8	64.0	21	15	US-10-267-217-82
4	12.8	64.0	21	15	US-10-283-582-33
5	12.8	64.0	25	15	US-10-215-112-3452
6	12.6	63.0	25	15	US-10-098-263B-25322
7	12.6	63.0	25	15	US-10-098-263B-94279
8	12.4	62.0	20	16	US-10-289-762-1851
9	12.4	62.0	24	10	US-09-940-185-1813
10	12.2	61.0	20	13	US-10-215-821-45
11	12.2	61.0	22	15	US-10-131-827-9031
12	12.2	61.0	23	15	US-10-091-841-14
13	12	60.0	23	10	US-09-892-949-6
14	12	60.0	25	13	US-10-358-228-12

C 15	12	60.0	25	15	US-10-098-263B-43779	Sequence 43779, A
C 16	11.8	59.0	20	16	US-10-190-366-23	Sequence 23, Appl
C 17	11.8	59.0	20	16	US-10-190-366-86	Sequence 86, Appl
C 18	11.8	59.0	20	16	US-10-190-366-220	Sequence 220, App
C 19	11.8	59.0	20	16	US-10-190-366-283	Sequence 283, App
C 20	11.8	59.0	20	17	US-10-211-908-74	Sequence 74, Appl
C 21	11.8	59.0	21	10	US-09-902-563-29	Sequence 29, Appl
C 22	11.8	59.0	21	15	US-10-096-255-29	Sequence 29, Appl
C 23	11.8	59.0	22	8	US-08-812-93A-42	Sequence 42, Appl
C 24	11.8	59.0	22	11	US-09-774-681-42	Sequence 319, App
C 25	11.8	59.0	22	13	US-10-262-511-319	Sequence 147, App
C 26	11.8	59.0	22	13	US-10-187-978-147	Sequence 8231, Ap
C 27	11.8	59.0	25	15	US-10-215-112-8251	Sequence 60, Appl
C 28	11.6	58.0	20	16	US-10-296-540-60	Sequence 14, Appl
C 29	11.6	58.0	21	13	US-10-431-599-14	Sequence 56871, A
C 30	11.6	58.0	25	15	US-10-098-263B-56871	Sequence 76311, A
C 31	11.6	58.0	25	15	US-10-098-263B-76311	Sequence 76312, A
C 32	11.6	58.0	25	15	US-10-098-263B-80220	Sequence 80220, A
C 33	11.6	58.0	18	15	US-10-098-263B-80220	Sequence 14, Appl
C 34	11.4	57.0	20	9	US-09-734-846-54	Sequence 54, Appl
C 35	11.4	57.0	20	9	US-09-734-846-55	Sequence 55, Appl
C 36	11.4	57.0	20	9	US-09-734-846-56	Sequence 56, Appl
C 37	11.4	57.0	20	9	US-09-734-846-57	Sequence 57, Appl
C 38	11.4	57.0	20	9	US-09-745-317-83	Sequence 83, Appl
C 39	11.4	57.0	20	9	US-09-745-317-87	Sequence 87, Appl
C 40	11.4	57.0	20	9	US-09-953-562-23	Sequence 23, Appl
C 41	11.4	57.0	20	15	US-10-302-262-54	Sequence 54, Appl
C 42	11.4	57.0	20	15	US-10-302-262-55	Sequence 55, Appl
C 43	11.4	57.0	20	15	US-10-302-262-56	Sequence 56, Appl
C 44	11.4	57.0	20	15	US-10-302-262-57	Sequence 57, Appl
C 45	11.4	57.0	20	15	US-10-302-262-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1
US-10-210-479-73
; Sequence 73, Application US/10210479
; Publication No. US20040023380A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR 6 EXPRESSIC
; FILE REFERENCE: RTS-0385
; CURRENT APPLICATION NUMBER: US/10/210,479
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-479-73

Query Match 66.0% Score 13.2; DB 17; Length 20;
Best Local Similarity 83.3% Pred. No. 5.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0;

Cy 3 GAATGCCACTTGGACT 20
Db 1 GAAGGCACCTTGGACT 18

RESULT 2
US-10-210-479-119/c
; Sequence 119, Application US/10210479
; Publication No. US20040023380A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR 6 EXPRESSIC

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FILE REFERENCE: RTS-0385
CURRENT APPLICATION NUMBER: US/10/210.479
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 123
SEQ ID NO 119
LENGTH: 20
TYPE: DNA
ORGANISM: H. sapiens
FEATURE:
US-10-210-479-119
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Query Match      66.0%; Score 13.2; DB 17; Length 20;
Best Local Similarity 83.3%; Pred. No. 5.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      3 GAATGGCCACTTTGGCACT 20
DB      20 GAATGGCCACTTTGGCACT 3
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RESULT 3

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US-10-267-217-22
Sequence 22, Application US/10267217
Publication No. US20030105318A1
GENERAL INFORMATION:
APPLICANT: Borowsky, Beth E.
APPLICANT: Ogozalek, Kristine L.
APPLICANT: Jones, Kenneth A.
TITLE OF INVENTION: DNA Encoding SNORF33 Receptor
FILE REFERENCE: 59338A
CURRENT APPLICATION NUMBER: US/10/267.217
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: US/09/413.433
PRIOR FILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: 09/322.257
PRIOR FILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patent In Ver. 2.0 - Beta
SEQ ID NO 22
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer/probe
US-10-267-217-22
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Query Match      64.0%; Score 12.8; DB 15; Length 21;
Best Local Similarity 87.5%; Pred. No. 8.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      5 ATGGCCACTTTGGCACT 20
DB      2 ATGGCCACTTTGGCACT 17
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RESULT 4

```
US-10-293-582-33
Sequence 33, Application US/10293582
Publication No. US20030175253A1
GENERAL INFORMATION:
APPLICANT: Akil, Huda
APPLICANT: Bunney, William E.
APPLICANT: Burke, Sharon
APPLICANT: Choudary, Prabhakara V.
APPLICANT: Cox, David R.
APPLICANT: Evans, Simon
APPLICANT: Jones, Edward G.
APPLICANT: Li, Jun
APPLICANT: Lopez, Juan F.
APPLICANT: The Trustees of The Leland Stanford Junior University
TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating
FILE REFERENCE: 020885-000210US
```

```
CURRENT APPLICATION NUMBER: US/10/293.582
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 60/339,252
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 33
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: reverse PCR
US-10-293-582-33
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Query Match      64.0%; Score 12.8; DB 15; Length 21;
Best Local Similarity 87.5%; Pred. No. 8.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY      5 ATGGCCACTTTGGCACT 20
DB      2 ATGGCCACTTTGGCACT 17
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```
RESULT 5
US-10-215-112-3452
Sequence 3452, Application US/10215112
Publication No. US20030082596A1
GENERAL INFORMATION:
APPLICANT: Michael, Maltman
TITLE OF INVENTION: Method of Genetic Analysis of Probes:
FILE REFERENCE: 3119
CURRENT APPLICATION NUMBER: US/10/215.112
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 14936
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3452
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-3452
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Query Match      64.0%; Score 12.8; DB 15; Length 25;
Best Local Similarity 87.5%; Pred. No. 8.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      2 TGAATGGCCACTTTGC 17
DB      1 TGAATGGCCACTTTTC 16
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```
RESULT 6
US-10-098-263B-25322/c
Sequence 25322, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098.263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 25322
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-25322
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Query Match      63.0%; Score 12.6; DB 15; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GTGATGGCCACTTTGCAC 19
DB      19 GTTAACTCCACTTTGCAC 1

RESULT 7
US-10-098-263B-94279/c
; Sequence 94279, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mitteran, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 94279
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-94279

Query Match      63.0%; Score 12.6; DB 15; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TGAATGGCCACTTTGCAC 20
DB      25 TGAACAGGCACTTTGCAC 7

RESULT 8
US-10-289-762-1851
; Sequence 1851, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1851
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-1851

Query Match      62.0%; Score 12.4; DB 16; Length 20;
Best Local Similarity 92.9%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GGCCACTTTGCAC 20
DB      2 GGCCACTTTGCAC 15

RESULT 9
US-09-940-185-3813/c
; Sequence 3813, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin

Query Match      62.0%; Score 12.4; DB 10; Length 24;
Best Local Similarity 92.9%; Pred. No. 1.4e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 GAATGGCCACTTTG 16
DB      23 GAATGGCCACTTTG 10

RESULT 10
US-10-215-821-45
; Sequence 45, Application US/10215821
; Publication No. US20040029274A1
; GENERAL INFORMATION:
; APPLICANT: Jacquelline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF EDG5 EXPRESSION
; FILE REFERENCE: R15-0155
; CURRENT APPLICATION NUMBER: US/10/215,821
; CURRENT FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 111
; SEQ ID NO 45
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-215-821-45

Query Match      61.0%; Score 12.2; DB 13; Length 20;
Best Local Similarity 92.4%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 AATGGCCACTTTGCAC 20
DB      3 AATGGCCACTTTGCAC 19

RESULT 11
US-10-131-827-9031/c
; Sequence 9031, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fiy, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMM
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
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PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9031
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-10-131-827-9031

Query Match 61.0%; Score 12.2; DB 16; Length 22;
Best Local Similarity 82.4%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGATGGCCACTTGGCA 18
DB 17 TGAATGTCACACTGCA 1

RESULT 12
US-10-091-841-14/c
Sequence 14, Application US/10091841
Publication No. US20030150010A1
GENERAL INFORMATION:
APPLICANT: Cho, Myeong-Je
APPLICANT: Del Val, Greg
APPLICANT: Caillaud, Maxime
APPLICANT: Lemaux, Peggy G.
APPLICANT: Buchanan, Bob B.
TITLE OF INVENTION: Barley Gene for Thioresdoxin and
TITLE OF INVENTION: NADP-thioresdoxin Reductase
FILE REFERENCE: 2001-0701.30
CURRENT FILING DATE: 2002-03-05
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/540,014
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 60/127,138
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: US 60/169,162
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 60/177,740
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 60/177,739
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: degenerative primer
US-10-091-841-14

Query Match 61.0%; Score 12.2; DB 15; Length 23;
Best Local Similarity 57.9%; Pred. No. 1.8e+04;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGATGGCCACTTGGCC 19
DB 21 GTGATGGCGCYTSGAC 3

RESULT 13
US-09-892-949-6/c
Sequence 6, Application US/09892949
Publication No. US20030096339A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Presnell, Scott R.
APPLICANT: Gao, Zeren
APPLICANT: Whitmore, Theodore E.

APPLICANT: Kulper, Joseph L.
APPLICANT: Maurer, Mark F.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
FILE REFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer ZC27898
US-09-892-949-6

Query Match 60.0%; Score 12; DB 10; Length 23;
Best Local Similarity 75.0%; Pred. No. 2.2e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTGATGGCCACTTGGCACT 20
DB 22 GTGATGGCTGCTGGCT 3

RESULT 14
US-10-358-228-12/c
Sequence 12, Application US/10358228
Publication No. US20030211578A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc. et al.
TITLE OF INVENTION: Interferon Receptor HKAEF92
FILE REFERENCE: PF465C1
CURRENT APPLICATION NUMBER: US/10/358,228
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: 09/453,569
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 09/326,216
PRIOR FILING DATE: 1999-06-03
PRIOR APPLICATION NUMBER: 60/088,185
PRIOR FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Primer Bind
OTHER INFORMATION: Synthetic primer complementary to the INFR-HKAEF92 protein;
OTHER INFORMATION: Includes a NdeI restriction site.
US-10-358-228-12

Query Match 60.0%; Score 12; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GAATGGCCACTT 14
DB 25 GAATGGCCACTT 14

RESULT 15
US-10-098-263B-43779/c
Sequence 43779, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 00:43:42 ; Search time 2406 Seconds
(without alignments)
248.231 Million cell updates/sec

Title: US-09-693-205A-47

Perfect score: 20

Sequence: 1 gtgaatgaccacttgcact 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 22888

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: em_estda:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estum:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11.8	59.0	24	28	A2443113 1M0237G08
2	11.8	59.0	24	28	A2498795 1M0336D16
3	11.6	58.0	19	28	A2510142 1M0354P20
4	11.4	57.0	25	29	TA350F090 AL496767 T. brucei

C	5	11.2	56.0	25	A1344221 tc02h03.x
C	6	11.2	56.0	25	A2510116 1M0354H21
C	7	10.4	52.0	20	A2514794 1M0361C13
C	8	10.4	52.0	22	A2794867 2M0048015
C	9	10.4	52.0	25	A2404619 1M0173L20
C	10	10.4	52.0	25	TA237D080 AL481334 T. brucei
C	11	10.2	51.0	19	A2538825 1M0101J20
C	12	10.2	51.0	19	A2591963 1M0402P23
C	13	10.2	51.0	22	CE269578 FCYLC01d7
C	14	10.2	51.0	24	A2837385 2M0132E10
C	15	10.2	51.0	25	A2598351 1M0413D12
C	16	10.0	50.0	25	A2532290 1M0090M10
C	17	9.8	49.0	20	A2773092 1M0584K20
C	18	9.8	49.0	20	A2784682 2M0027B07
C	19	9.8	49.0	21	A2657958 1M0534E02
C	20	9.8	49.0	21	A2814489 2M0082C14
C	21	9.6	48.0	20	A2802430 2M0061G14
C	22	9.6	48.0	23	A0934937 D11B068
C	23	9.6	48.0	25	A2767331 1M0566N19
C	24	9.4	47.0	15	B0511821 EST619236
C	25	9.4	47.0	19	A2514722 1M0361C10
C	26	9.4	47.0	21	A2447803 1M0245F08
C	27	9.4	47.0	21	A2865515 2M0175U07
C	28	9.4	47.0	24	CA967214 CcL01a03
C	29	9.4	47.0	24	TA100C010 AL459332 T. brucei
C	30	9.4	47.0	25	AA948130 on51c12.s
C	31	9.4	47.0	25	AI181406 UC59404.r
C	32	9.2	46.0	20	A0255294 A0235294
C	33	9.2	46.0	20	A2317291 1M0035N10
C	34	9.2	46.0	20	A2630221 1M0483K12
C	35	9.2	46.0	20	A2651800 1M0522N07
C	36	9.2	46.0	20	A2662792 1M0542P02
C	37	9.2	46.0	20	A2836069 2M0130U13
C	38	9.2	46.0	20	A2836069 2M0130U13
C	39	9.2	46.0	21	A2465773 1M0275T23
C	40	9.2	46.0	22	A2433553 1M0202N09
C	41	9.2	46.0	22	A2949397 2M0212D23
C	42	9.2	46.0	23	A2321517 1M0042C12
C	43	9.2	46.0	23	AZ807926 2M0071C09
C	44	9.2	46.0	24	A2845345 2M0145B09
C	45	9.2	46.0	25	AI499484 t002a09.x
C	46	9.2	46.0	25	AZ408539 1M0179G17

ALIGNMENTS

RESULT 1
LOCUS A2443113
DEFINITION 1M0237G08R Mouse 10kb plasmid UGCM library Mus musculus genomic
clone UGCM1M0237G08 R, genomic survey sequence.
ACCESSION A2443113
VERSION A2443113.1 GI:10590773
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

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Page 2

Email: ddum@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0237 row: G column: 08
Seq primer: CACACGAGAAACGCTTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers

FEATURES

source

1. 24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0237G08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 59.0%; Score 11.8; DB 28; Length 24;
Best Local Similarity 86.7%; Pred. No. 9.3e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AATGCCACTTTGCA 18
| | | | | | | | | | | | | | | | | | | | | |
Db 4 AATGCCACTTTGAA 18

RESULT 2
AZ498795 24 bp DNA linear GSS 05-OCT-2000
LOCUS 1M033616F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG1M033616 F, genomic survey sequence.
ACCESSION AZ498795
VERSION AZ498795.1 GI:10676983
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., StC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddum@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0236 row: D column: 16
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers

FEATURES

source

1. 24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M033616"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 59.0%; Score 11.8; DB 28; Length 24;
Best Local Similarity 86.7%; Pred. No. 9.3e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AATGCCACTTTGCA 18
| | | | | | | | | | | | | | | | | | | | | |
Db 1 AATGCCACTTTGTA 15

RESULT 3
AZ510142/c 19 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0354P20F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG1M0354P20 F, genomic survey sequence.
ACCESSION AZ510142
VERSION AZ510142.1 GI:10691458
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., StC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0354 row: P column: 20
 Seq primer: CGTGTAAACGACGGCGCACT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES

source

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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UTGCM0354P20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid library"
 /note="Vector: pMD42nv; purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 58.0%; Score 11.6; DB 28; Length 19;
 Best Local Similarity 77.8%; Pred. No. 1e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GTGAATGGCACTTGA 18
 18 GTTAATGTCACATTGTA 1

RESULT 4

TA350F09Q 25 bp DNA linear GSS 13-DEC-2000
 LOCUS T. brucei sheared genomic DNA clone 350F09, reverse sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AL496767
 VERSION AL496767.1 GI:11870376
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 25)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridgeshire CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nhlesanger@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small

COMMENT

TITLE

AUTHORS

REFERENCE

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nhlesayer@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers

FEATURES

source

1..25
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="350F09"

ORIGIN

Query Match 57.0%; Score 11.4; DB 29; Length 25;
 Best Local Similarity 92.3%; Pred. No. 1.5e+05;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 AATGCCCACTTTG 16
 13 AATGCCCACTTTG 25

RESULT 5

AI1344221/c 25 bp mRNA linear EST 08-APR-1999
 LOCUS tco2h03.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:2062709 3'
 DEFINITION similar to WP:CG9H.5 CE04231 ZINC-FINGER TRANSCRIPTION REGULATOR
 ;, mRNA sequence.
 AI1344221
 AI1344221.1 GI:4081427

EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgsaps-remail.nih.gov
 Tissue Procurement: Ian Kirsch, M.D., Michael R. Emmert-Buck,
 M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CCAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 www.bio.lnl.gov/bhrp/image/image.html

JOURNAL

COMMENT

Trace considered overall poor quality
 Insert Length: 462 Std Error: 0.00
 Seq primer: -40UP from Gdbco
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

1..25
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2062709"
 /tissue_type="colon tumor, RER+"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Col6"
 /note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
 modified polylinker; Site 1: Not I; Site 2: Eco RI;
 Plasmid DNA from the normalized library NCI-CCAP Col6 was
 prepared, and ss circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library

1. .25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0334H21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, λ -resistant, F-"
/clone_library="Mouse 10kb plasmid UGCG1M library"
/note="Vector: pMD42uv". Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repeated with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
ligated DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into

1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGUGM0361C13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid UGUGM library"
/note="(Vector: PWD4inv). Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passages through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative of
pMD24 (g1147311[g9]A12507.1), a copy-number was ligated to
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into

ORIGIN

chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 52.0%; Score 10.4; DB 28; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.3e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATGGCCACTTGG 16

Db 17 ATGGCCACTTGG 6

RESULT 8
A2794867 22 bp DNA linear GSS 16-FEB-2001

LOCUS
DEFINITION
2M0048015R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0048015 R, genomic survey sequence.

ACCESSION
A2794867
A2794867.1 GI:12941279

VERSION
KEYWORDS
GSS.
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

JOURNAL

Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

COMMENT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0048 row: 0 column: 15
Seq primer: CACACGAGAAACGCTACGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES

source

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0048015"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

ORIGIN

chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 52.0%; Score 10.4; DB 28; Length 22;
Best Local Similarity 91.7%; Pred. No. 4.5e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TGGCCACTTGGC 17

Db 6 TGGCCACTTGGC 17

RESULT 9
A2404619 25 bp DNA linear GSS 03-OCT-2000

LOCUS
DEFINITION
1M0173U20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0173U20 F, genomic survey sequence.

ACCESSION
A2404619
A2404619.1 GI:10528632

VERSION
KEYWORDS
GSS.
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

JOURNAL

Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

COMMENT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0173 row: 1 column: 20
Seq primer: CGTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers

FEATURES

source

1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0173U20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

Page 6

ACCESSION	AZ591963
VERSION	AZ591963.1
KEYWORDS	GI:11714153
SOURCE	Mus musculus (house mouse)
LOCUS	1M0402P23F Mouse 10kb plasmid tUGC1M library Mus genomic clone tUGC1M0402P23 F, genomic survey sequence.
DEFINITION	19 bp DNA linear GSS 13-DEC-2000
FEATURES	
REMARKS	
REFERENCE	
COMMENTARY	
RESIDUE_12	

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0402 row: P column: 23
Seq primer: CGTGTAAACGACGCCACGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="MUGCM0402P23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid UGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114[gb]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 51.0%; Score 10.2; DB 28; Length 19;
Best Local Similarity 80.0%; Pred. No. 5.3e+05;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 TGGCCACTTGGCACT 20
|||||
DB 1 TGGCTACATGCTCT 15
|||||

RESULT 13
CF269578 22 bp mRNA linear EST 13-AUG-2003
CF269578
DEFINITION Fcylcoid755 Fragilariopsis cylindrus SMART cDNA library (Clontech)
ACCESSION CF269578
VERSION CF269578.1 GI:33631465
KEYWORDS EST.
SOURCE Fragilariopsis cylindrus

ORGANISM Fragilariopsis cylindrus
Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
Bacillariophycidae; Bacillariales; Bacillariaceae; Fragilariopsis.

REFERENCE 1 (bases 1 to 22)
AUTHORS Mock, T. and Valentin, K.
EST analysis of freezing tolerance in the Antarctic diatom
Fragilariopsis cylindrus: Detection of numerous cold adaption
related genes and gene transfer events
Unpublished (2003)

JOURNAL Contact: Mock T
Biological Oceanography
Alfred-Wegener-Institute for Polar and Marine Research
Am Handelshafen 12, D-27570 Bremerhaven, Germany
Tel: +49 471 4831 1893
Fax: +49 471 4831 1425
Email: tmock@awi-bremerhaven.de
sequence with unknown function
PCR primers
FORWARD: 5'lambdaT-ripLEX2
BACKWARD: 3'lambdaT-ripLEX2
Seq primer: ctgggaagcgccacatgtgtgtgt.
Location/Qualifiers

FEATURES
source
1..22
/organism="Fragilariopsis cylindrus"
/mol_type="mRNA"
/strain="Antarctic"
/db_xref="taxon:186039"
/clone="Antarctic"
/clone_id="Fragilariopsis cylindrus SMART cDNA library
(Clontech)"
/note="Vector: Pripriplex2; total polyA was used for
first-strand synthesis with SMART IV oligos and CDS
III/3'PCR primer. Double strand cDNA synthesis was done by
LD PCR using the following program: 95oc for 5 min
denaturation and subsequent 20 cycles at 95oc (2min) and
68oc (6min). After SfiI digestion the cDNA was
fractionated with CHROMA Spin-400 columns. These cDNAs
were ligated overnight into Pripriplex2 vectors."

ORIGIN
Query Match 51.0%; Score 10.2; DB 14; Length 22;
Best Local Similarity 80.0%; Pred. No. 5.7e+05;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 TGGCCACTTGGCACT 20
|||||
DB 1 TGGCCACTTGGCCT 15
|||||

RESULT 14
AZ837385 24 bp DNA linear GSS 20-FEB-2001
AZ837385
DEFINITION 2M0132E10r Mouse 10kb plasmid UGCM library Mus musculus genomic
clone UGCM2M0132E10 R, genomic survey sequence.

ACCESSION AZ837385
VERSION AZ837385.1 GI:13007293
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0132 row: E column: 10
Seq primer: CACACAGGAACACTATGACC
Class: plasmid ends
High quality sequence stop: 24.

FEATURES

Location/Qualifiers
1. .24
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0132E10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 51.0%; Score 10.2; DB 28; Length 24;
Best Local Similarity 80.0%; Pred. No. 5.9e+05;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 TGAATGCCCACTTTG 15
Db 2 TGAATGCCCACTTTG 16

RESULT 15
AZ598351
LOCUS
DEFINITION
1M0413D12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0413D12 F, genomic survey sequence.
ACCESSION
AZ598351
VERSION
AZ598351.1 GI:11720541
SOURCE
GSS.
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D. Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0413 row: D column: 12
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.

FEATURES

Location/Qualifiers
1. .25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0413D12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 51.0%; Score 10.2; DB 28; Length 25;
Best Local Similarity 80.0%; Pred. No. 6e+05;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 TGAATGCCCACTTTG 16
Db 2 TGAATGCCCACTTTG 16

Search completed: May 27, 2004, 02:22:36
Job time : 2410 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

1 nucleic - nucleic search, using sw model

in on: May 26, 2004, 20:25:31 ; Search time 56.2249 Seconds
(without alignments)
4935.099 Million cell updates/sec

file: US-09-693-205A-7_COPY_1_500

object score: 500

sequence: 1 atgattacaggagaccat.....gcagaaattgtgtaatacaaa 500

oring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

sarched: 682709 seqs, 277475446 residues

total number of hits satisfying chosen parameters: 1365418

inimum DB seq length: 0

aximum DB seq length: 2000000000

ost-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase : Issued Patents NA:*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PTCUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
C 1	42.4	8.5	1407	4	US-09-328-352-1897
C 2	37.2	7.4	39003	4	US-09-396-002-21
C 3	36	7.2	1404	4	US-09-134-000C-2362
C 4	35.8	7.2	768	4	US-09-134-000C-1137
C 5	35.6	7.1	516	4	US-09-601-198-79
C 6	35.6	7.1	3129	3	US-09-387-695-1
C 7	35.6	7.1	19446	4	US-08-961-527-51
C 8	35.4	7.1	1664976	4	US-08-916-421B-1
C 9	35.2	7.0	832	4	US-09-621-976-2813
C 10	34.8	7.0	658	3	US-09-328-111-775
C 11	34.8	7.0	842	4	US-08-956-171B-808
C 12	34.2	6.8	3456	1	US-08-190-687B-24
C 13	34.2	6.8	4307	1	US-08-190-687B-7
C 14	34	6.8	392000	4	US-10-027-983-11
C 15	34	6.8	1664976	4	US-08-916-421B-1
C 16	33.6	6.7	819	4	US-09-601-198-45
C 17	33.6	6.7	1746	4	US-09-107-532A-3181
C 18	33.2	6.6	1308	4	US-09-601-198-3
C 19	33.2	6.6	5058	4	US-09-889-595-1
C 20	33.2	6.6	6479	2	US-08-649-046-3
C 21	33	6.6	1254	4	US-09-321-017B-1016
C 22	32.8	6.6	853	2	US-08-179-557-19
C 23	32.6	6.5	580073	4	US-08-545-528D-1
C 24	32.6	6.5	640681	4	US-09-780-988-1
C 25	32.4	6.5	279	4	US-09-601-198-25
C 26	32.4	6.5	501	4	US-09-328-352-3153
C 27	32.4	6.5	1590	4	US-09-403-942F-70

28 32.4 6.5 1590 4 US-09-403-942F-71 Sequence 71, Appl
c 29 32.4 6.5 1987 4 US-09-403-942F-67 Sequence 67, Appl
30 32.4 6.5 1987 4 US-09-403-942F-69 Sequence 69, Appl
31 32.4 6.5 3000 2 US-08-680-395-1 Sequence 1, Appl
32 32 6.4 149 1 US-08-629-929-4 Sequence 4, Appl
33 32 6.4 149 1 US-08-759-873-4 Sequence 4, Appl
34 32 6.4 180 3 US-09-004-113-13 Sequence 13, Appl
35 32 6.4 474 4 US-09-621-976-18033 Sequence 13, Appl
c 36 32 6.4 11832 2 US-08-416-603-1 Sequence 1, Appl
c 37 32 6.4 168575 4 US-09-426-290-1 Sequence 1, Appl
c 38 32 6.4 1830121 4 US-09-557-884-1 Sequence 1, Appl
c 39 32 6.4 1830121 4 US-09-643-990A-1 Sequence 1, Appl
40 31.8 6.4 1419 1 US-08-242-098-39 Sequence 39, Appl
41 31.6 6.3 400 4 US-08-956-371E-3940 Sequence 3940, Ap
42 31.6 6.3 582 4 US-08-338-352-47 Sequence 47, Appl
c 43 31.6 6.3 1298 4 US-08-971-089-1 Sequence 1, Appl
44 31.6 6.3 2016 3 US-09-132-118-1 Sequence 1, Appl
45 31.6 6.3 2106 3 US-08-923-511-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-328-352-1897/c
; Sequence 1897, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328.352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1897
; LENGTH: 1407
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1897

Query Match 8.5%; Score 42.4; DB 4; Length 1407;
Best Local Similarity 54.5%; Pred. No. 0.0095;
Matches 85; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 306 TTTTAGAGTGAATCTGAACACAGCTTCCAGATTTTTCAGAGATTTGACAAAC 365
Db 735 TTGGAAGCATGTAAACACAGCATTTCTGCATCAAAATCAGGAACCTAAAC 676
QY 366 TTGGAGGTTTGTCTTAAATAATAGATGATCTATACAACTCCGCTTATTAAAAAT 425
Db 675 TTGTAGGTTTGTGCTGACGCTCAAGTTTAAATTTCTGCTTCAGTCACTAAACCTAATGT 616
QY 426 ATATTCAATCACTTACCAGTCTCTTTTTCGAGA 461
Db 615 ACCTTCCACCACCAATAACAAATGCTGTAATGCATA 580

RESULT 2
US-09-596-002-21
; Sequence 21, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
; APPLICANT: Patterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PM-0008-4 US
; CURRENT APPLICATION NUMBER: US/09/596.002
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 41


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; SOFTWARE: PERL Program
; SEQ ID NO 21
; LENGTH: 39003
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte template ID No. 6632636 21
; PUBLICATION INFORMATION:
US-09-596-002-21

Query Match      7.4%; Score 37.2; DB 4; Length 39003;
Best Local Similarity 52.6%; Pred. No. 1;
Matches 81; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 291 TTCCATCGTTAGTCATTTTAGACGATGAATCTGAAGCACAGCTTCCAGAAATTTTAGCAG 350
Db 22598 TTATCTGGCTTGGCATCAAAACTCTGGTTTAAAGCACCTGTCACAGTTTAAAGAAG 22657
QY 351 ACATTGTACAAAACCTTGGAGGGTTTGCTTTAAATAATATAGATGCTCTATACAAATC 410
Db 22658 AAGATGTTTAAATCTTAAATAAAATATCCTTAAATAAAATATCCTTAAATAAAATA 22717
QY 411 CGCTTATTAATAAATATATTCATTCACCATTAAC 444
Db 22718 TCCTTAATAAATAATCTCTTAAATAAATAATC 22751

RESULT 3
US-09-134-000C-2362/c
; Sequence 2362, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynx Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2362
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2362

Query Match      7.2%; Score 36; DB 4; Length 1404;
Best Local Similarity 53.6%; Pred. No. 0.66;
Matches 75; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 341 TTTTACGACATTTGTACAAAACCTGGAGGGTTTGCTTTAAAAAATTAGATGCATCT 400
Db 1199 TTTTACGCTTGTCCATAATAAATCTGAAGGTTTATAACACAAATATTTGATGGAAT 1140
QY 401 ATACAACATCCGTTATTAATAAATATATTCATTCACCAATACCAAGTCTGTTTTCGAG 460
Db 1139 GCATGTGCTCAAACTAAATGATTAATTAATTCACCTTTAGTACCATCTTTATAACAG 1080
QY 461 ATAATGGAGAGATGCCAT 480
Db 1079 AAAATGAATACCAATAAAT 1060

RESULT 4
US-09-134-000C-1137
; Sequence 1137, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynx Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1137
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1137

Query Match      7.2%; Score 35.8; DB 4; Length 768;
Best Local Similarity 51.6%; Pred. No. 0.59;
Matches 82; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 305 ATTATTAGACGATGAATCTGAAGCACAGCTTCCAGAAATTTTAGCAGACATTTACAAAA 364
Db 430 ATTATTACATGCTATACGAGAAAAACAGCAAGAAATTTGGAAACAAATTAACAAGCT 489
QY 365 CTTCGAGGGTTTGCTTTAAAAAATTAGATGCATCTATACAAATCCGCTTATTAATAAAA 424
Db 490 GAACCAAGTTTGCTTTGTAGCATTAGTTCCAGCAAGAGAGATTTTGTGGACAA 549
QY 425 TATATTCATTCACCAATACCAAGTCTGTTTTCAGATA 463
Db 550 ACAATTGATCACCTGACAGCTAATGTATTTTAGACGTA 588

RESULT 5
US-09-601-198-79
; Sequence 79, Application US/09601198
; Patent No. 6531583
; GENERAL INFORMATION:
; APPLICANT: Cassell, Gail H.
; APPLICANT: Chen, Ellison Y.
; APPLICANT: Glass, Jennifer S.
; APPLICANT: Heiner, Cheryl R.
; APPLICANT: Lefkowitz, Elliot
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING URAPLASMA
; FILE REFERENCE: UAB-13452/22
; CURRENT APPLICATION NUMBER: US/09/601,198
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/073,189
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 79
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
US-09-601-198-79

Query Match      7.1%; Score 35.6; DB 4; Length 516;
Best Local Similarity 48.5%; Pred. No. 0.58;
Matches 98; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 264 CATGTGTGAATCATATTAGATTCAGATTCAGATTCATTCATTTTAGCAGTGAATCTG 323
Db 77 CAACTGTGATTTAATTAATATATGAAGAAATTAATGCGATCAGTTTATTTGATAATAAT 136
QY 324 AAGCAGCTTCCAGAAATTTTAGCAGACATTTGACAAAACTTGGAGGGTTTGCCTTA 383
Db 137 TAGGTTTGAATCAGAGGTTTATTAGATTTTCTTAAAAAATTTACATTAGCTTTTGAAA 196
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384 AAAAATAGATGATCTATACACATCCGCTTATTAAAAATATATTCATTCACCATTTAC 443
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197 AAAAATAGATGATCTATACACATCCGCTTATTAAAAATATATTCATTCACCATTTAC 256
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444 CAAAGTGTCTTTTGCAGATAAT 465
257 CAAACTATATGATTCAT 278
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SULT 6
-09-387-695-1/c
Sequence 1, Application US/09387695
Patent No. 6280990
GENERAL INFORMATION:
APPLICANT: May, Earl
APPLICANT: Van Horn, Stephanie
APPLICANT: Warren, Patrick V.
APPLICANT: Warren, Richard L.
TITLE OF INVENTION: dnaE
FILE REFERENCE: GM10237
CURRENT APPLICATION NUMBER: US/09/387,695
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 3129
TYPE: DNA
ORGANISM: Streptococcus pneumoniae
;-09-387-695-1

Query Match 7.1%; Score 35.6; DB 3; Length 3129;
Best Local Similarity 51.9%; Pred. No. 1.2;
Matches 80; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

106 GATTGTTCAATGGTATCCATTTGATGAAACAGAAATCACCCATCTGTTTCATGGCTTAA 165
|||||
2543 GATTCCTGCCAACTATAAATAGCATCTCCAAACAAACTTCCCAACTCTTTCACAAATTC 2484
|||||
166 GATGTTTGGAAAAATCTTTATATACATTTTTCAGAGGATTTGATCTTATTTGATGAGAT 225
|||||
2483 AATAGATTAGCTAAGTTATTAATACCTTTTGGACGATTTTTCATTAATGATGAGAT 2424
|||||
226 GCACCTATCCCAAGCACTATCTAGAGGAGGT 259
|||||
2423 CCAACTTTTACCAAGGTTCTAGCAGAGGAGGT 2390
|||||

3SULT 7
-08-961-527-51/c
Sequence 51, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brooks, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 19446 base pairs
TYPE: nucleic acid
STRANDEDNESS: Double
TOPOLOGY: linear
US-08-961-527-51

Query Match 7.1%; Score 35.6; DB 4; Length 19446;
Best Local Similarity 51.9%; Pred. No. 2.3;
Matches 80; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

106 GATTGTTCAATGGTATCCATTTGATGAAACAGAAATCACCCATCTGTTTCATGGCTTAA 165
|||||
17811 GATTCCTGCCAACTATAAATAGCATCTCCAAACAAACTTCCCAACTCTTTCACAAATTC 17752
|||||
166 GATGTTTGGAAAAATCTTTATATACATTTTTCAGAGGATTTGATCTTATTTGATGAGAT 225
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17751 AATAGATTAGCTAAGTTATTAATACCTTTTGGACGATTTTTCATTAATGATGAGAT 17692
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226 GCACCTATCCCAAGCACTATCTAGAGGAGGT 259
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17691 CCAACTTTTACCAAGGTTCTAGCAGAGGAGGT 17658
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RESULT 8
US-08-916-421B-1
Sequence 1, Application US/08916421B
Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
TITLE OF INVENTION: jannaschii
Patent No. 6503729
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
FEATURE:
NAME/KEY: misc feature
LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature

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; NAME/KEY: misc feature
; OTHER INFORMATION: n equals a, t, c, or g
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; OTHER INFORMATION: n equals a, t, c, or g
; LOCATION: (191995)..(191995)
; NAME/KEY: misc feature
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; LOCATION: (312837)..(312837)
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; OTHER INFORMATION: n equals a, t, c, or g
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; NAME/KEY: misc feature
; OTHER INFORMATION: n equals a, t, c, or g
; LOCATION: (674435)..(674435)

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; OTHER INFORMATION: n equals a, t, c, or g
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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1349491)..(1349491)
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; LOCATION: (1602912)..(1602912)
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; NAME/KEY: misc feature
; LOCATION: (1603734)..(1603734)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1637998)..(1637998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1664854)..(1664854)
; OTHER INFORMATION: n equals a, t, c, or g
; US-08-916-421B-1

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Query Match 7.1%; Score 35.4; DB 4; Length 1664976;

Best Local Similarity 54.1%; Pred.No.14;

Matches 72; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 102 AATTCATTGTTCAATGGTATCCATTGATGAAACAGAAATCACCACCTCTGTTTCATGCG 161

DB 408286 AATAGATATGCTAACTATCCATCGAGATTACAAATGATCATGTTTGTGTTATC 408345

162 TTAAGATGGTTTGGAAAAATCTTTATATACATTTTTCAGAGATTGACCTTATTTGATG 221
408346 TTTTGTGAGCATATTTAATTTATTAAAGATTTTCTTAGTTTTCGAGTATATATATG 408405
222 AGATGCCACTTAT 234
408406 AGCAACACCTTTT 408418

RESULT 9
3-09-621-976-2813
Sequence 2813, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 235..399
S-09-621-976-2813

Query Match 7.0%; Score 35.2; DB 4; Length 832;
Best Local Similarity 11.0%; Pred. No. 0.91;
Matches 40; Conservative 158; Mismatches 166; Indels 0; Gaps 0;
Y 73 AGTAATGAATACATCTCGCTGGCAGAGATTTGATTTCAATGGTATCCATTTGATGA 132
b 13 AKCTWKKSWSYMYWKYMYKTYWRWRKKKAWKYKWTWTWYRYAMWGYKKKA 72
Y 133 AACAGAAATCACCATCTGTTTCATGGCTTAAGTGGTTTGGAAAAATCTTTATATACA 192
b 73 MCRTKTKKKKKGYMYWYWRWRSSYMAWTTWTGTYAYRSMYWRWYRCWKYKAYRK 132
Y 193 TTTTTCAGAGATTGACCTTTATTTGATGAGATGCCACTTATCCCGAGAACTATATACTAGA 252
b 133 TTCYSGKWTWKRWKANTTTWKKTYWATRYWYMYWYKWRWASWYCWYWGKARK 192
Y 253 GGAAGGTTCAGACATGTGTGGAACTCATATTAGACTCAGGATCCATGCTTAGTCACTTTAGA 312
b 193 WSTWRKRSYASARSARKCCYSCSWGMSWKYMWWRWGWATGAGMKAWPASCMWRRK 252
Y 313 CGATGATCTGAAGCAGAGCTTCCAGATTTTTCAGAGACATTTGACAAAAAATTTGGAGG 372
b 253 YAGSKTSYKSMWMCWTRSKYCTYKATWTGYCYKRGWGWGKRGWYASKYMKRWVW 312
Y 373 GTTTGTCTTTAAAAATATAGATCATCTATACATCCGCTTTATTTAAAAATATATATCA 432
b 313 CWARMYRYSTGRASWWRWRYTMMKWKYAWARAWEWYMWYWRACAAAAATATA 372
Y 433 TTCA 436
b 373 ATTA 376

RESULT 10
3-09-328-111-775
Sequence 775, Application US/09328111
Patent No. 6262333
GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.

APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie J.
APPLICANT: Catino, Theodore J.
APPLICANT: Derti, Adnan
APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 775
LENGTH: 658
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(658)
OTHER INFORMATION: n = A,T,C or G
US-09-328-111-775

Query Match 7.0%; Score 34.8; DB 3; Length 658;
Best Local Similarity 47.0%; Pred. No. 1.1;
Matches 108; Conservative 0; Mismatches 122; Indels 0; Gaps 0;
QY 193 TTTTTCAGAGATTGACCTTTATTTGATGAGATGCCACTTATCCCGAGAACTATATACTAGA 252
Db 139 TTTTTCATCTATATTAGTGCCTGTGTGATGGCATCTTTTCATCTAACACGCTGCTTTGAAGA 198
QY 253 GGAAGGTTCAGACATGTGTGGAATCTATTAGACTCAGGATTCATCGTTAGTCACTTTAGA 312
Db 199 TGATGATATCAGCGACGCTTGAAGAGAGTGTAGATCCTTTCAGATATAGAAATATACA 258
QY 313 CGATGATCTGAAGCAGACGCTTCCAGAAATTTTACGAGACATTTGTACAAAAAATTTGGAGG 372
Db 259 TGAAGAGCTTCAGCTTAAGATGAGAGAAATGATTGGGCCATTATAGATAAACTAGAAAAA 318
QY 373 GTTTGTCTTTAAAAATATAGATGCTATCTATACAACTCGCTTATATAAA 422
Db 319 GGTGGCTGTGAGAGGAGAGATAAAAAAATAAAACCTAAACCTGAATATGATATAA 368

RESULT 11
US-08-956-171E-808/c
Sequence 808, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.12
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 808:
SEQUENCE CHARACTERISTICS:
LENGTH: 842 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 808:
US-08-956-171E-808

Query Match 7.0%; Score 34.8; DB 4; Length 842;
Best Local Similarity 52.0%; Pred. No. 1.2;
Matches 78; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 351 ACATTGTCACAAAACCTGGAGGGTTGTCCTTAAAAAATTAGATGCATCATACAATC 410
Db 734 ATATTTGCCAAAATAATTAAAGTTTCTATCTCTTTTATGATTTGTAATCTCTATTT 675
QY 411 CGTTTATTAATAAATATATTCATTCACCATTAACCAAGTCTGTTTTGCAGATAATGGAGA 470
Db 674 ATCTATAGATAATTTTATTTATTTTTCATTCACCTTTTATAATTTTTTCTATCTGGAA 615
QY 471 AGATGCCATTGCAGAAATGCTGTAATCAA 500
Db 614 TTGCCCCCTTATTATAGATGCTCTTAACAAA 585

RESULT 12
US-08-190-687B-24
Sequence 24, Application US/08190687B
Patent No. 5760203
GENERAL INFORMATION:
APPLICANT: Wong, Gail L.
APPLICANT: Martin, George
APPLICANT: McCormick, Francis P.
APPLICANT: Rubinfeld, Bonnie
APPLICANT: O'Rourke, Edward C.
APPLICANT: Clark, Robin
TITLE OF INVENTION: GAP Gene Sequences
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,687B
FILING DATE: 02-FEB-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/774,644
FILING DATE: 11-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/260,807
FILING DATE: 21-OCT-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/230,761
FILING DATE: 10-AUG-1988
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 27527/31898
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 3456 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 100..2709
US-08-190-687B-24

Query Match 6.8%; Score 34.2; DB 1; Length 3456;
Best Local Similarity 55.5%; Pred. No. 3;
Matches 66; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 343 TTATACACACATTTTACAAAACCTGGAGGGTTGTCCTTAAAAAATTAGATGCATCTAT 402
Db 2100 TTATACACACATTTTGAACATATTCAGACCTTGTGAGAGAAATATTCATGCGTTTCA 2159
QY 403 ACAACATCGCTTTATTAATAAATATATTCATTCACCATTAACCAAGTCTGTTTTGCAGA 461
Db 2160 AATACTTCCACGACATTGAGATATATTTATGGGTGTTTACAGAAATCTGTTACGCATA 2218

RESULT 13
US-08-190-687B-7
Sequence 7, Application US/08190687B
Patent No. 5760203
GENERAL INFORMATION:
APPLICANT: Wong, Gail L.
APPLICANT: Martin, George
APPLICANT: McCormick, Francis P.
APPLICANT: Rubinfeld, Bonnie
APPLICANT: O'Rourke, Edward C.
APPLICANT: Clark, Robin
TITLE OF INVENTION: GAP Gene Sequences
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,687B
FILING DATE: 02-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/774,644

FILING DATE: 11-OCT-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/260,807
FILING DATE: 21-OCT-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/230,761
FILING DATE: 10-AUG-1988
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 27527/31898
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4307 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 119..3259
S-08-190-687B-7
Query Match 6.8%; Score 34.2; DB 1; Length 4307;
Best Local Similarity 55.5%; Pred. No. 3.3;
Matches 66; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
y 343 TTATGAGCATTTGACAAAACCTGGAGGGTTTCCTTAAAAAATTAGATGATCTAT 402
b 2650 TTTAACACACCTATTGAACATCTTTCAGAGCTTGGAGAAATATTCATGGCTTCAGA 2709
y 403 AGCAATCGCTTATTAAAAAATATTCATTCACCATTCACCAAGTGCTGTTTGCAGA 461
b 2710 AATCTTCCACGACATTGAGATATATTATGGGTGTTTACAGAAATCTGTTACGACATA 2768
ESULT 14
S-10-027-983-11/c
Sequence 11. Application US/10027983
Patent No. 6637162
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
APPLICANT: Mark P. Roach
TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR ALPHA EXPRESSION
FILE REFERENCE: RTS-0340
CURRENT APPLICATION NUMBER: US/10/027,983
CURRENT FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 11
LENGTH: 392000
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: 137740
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 137742
OTHER INFORMATION: unknown
NAME/KEY: misc feature
LOCATION: (138122)...(138221)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: unsure
LOCATION: 145507
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 151967
OTHER INFORMATION: unknown
NAME/KEY: misc_feature

LOCATION: (151967)...(1542066)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: unsure
LOCATION: 154217
OTHER INFORMATION: unknown
NAME/KEY: misc feature
LOCATION: (164037)...(164136)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc feature
LOCATION: (174657)...(174756)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc feature
LOCATION: (186224)...(186323)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc feature
LOCATION: (195242)...(195341)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: unsure
LOCATION: 202703
OTHER INFORMATION: unknown
NAME/KEY: misc feature
LOCATION: (202771)...(202870)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc feature
LOCATION: (206246)...(215602)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc feature
LOCATION: (218126)...(218225)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc feature
LOCATION: (220360)...(220459)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc feature
LOCATION: (222717)...(222816)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc feature
LOCATION: (223981)...(224080)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc feature
LOCATION: (227487)...(227586)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc feature
LOCATION: (230157)...(230256)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc feature
LOCATION: (232299)...(232398)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc feature
LOCATION: (236552)...(236651)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc feature
LOCATION: (238789)...(248788)
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: exon
LOCATION: (118288)...(119101)
OTHER INFORMATION: exon 1C
NAME/KEY: exon:intron junction
LOCATION: (151129)...(151130)
OTHER INFORMATION: exon 5:intron 5
NAME/KEY: exon:intron junction
LOCATION: (299248)...(299249)
OTHER INFORMATION: exon 9:intron 9
NAME/KEY: exon:intron junction
LOCATION: (348578)...(348579)
OTHER INFORMATION: exon 10:intron 10
NAME/KEY: intron
LOCATION: (348579)...(381838)
OTHER INFORMATION: intron 10
NAME/KEY: intron:exon junction
LOCATION: (386185)...(386186)
OTHER INFORMATION: intron 11:exon 12
US-10-027-983-11

Query Match 6.8%; Score 34; DB 4; Length 392000;
Best Local Similarity 57.5%; Pred No. 21;
Matches 61; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 114 AATGATATCCATTGATGAAGAAATCCATCTGTTTCATGCTTAAGATGTTT 173
DB 359266 AATGTTATTATATATCCCTGGAAGAGAAATCACTTACGCTGTTTAAACATCAGATGTTGTT 359207

QY 174 GGAATAATCTTTATATACATTTTTCAGAGGATTTGACTTTATTGGA 219
DB 359206 GAATAAATCATCTTGTATCAATCATGCTGATATATAGTTATTAA 359161

RESULT 15
US-08-916-421B-1/c
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; Patent No. 6503729
; FILE OF INVENTION: jannaschii
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (28257)..(28258)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84773)..(84773)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84808)..(84808)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84812)..(84812)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98120)..(98120)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98159)..(98159)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98239)..(98239)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98266)..(98266)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98343)..(98343)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (103398)..(103398)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (148948)..(148948)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (163385)..(163385)
; OTHER INFORMATION: n equals a, t, c, or g

; NAME/KEY: misc feature
; LOCATION: (191989)..(191989)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (191995)..(191995)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (231980)..(231980)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234187)..(234187)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234220)..(234220)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234814)..(234814)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (309198)..(309198)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (309418)..(309418)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (312837)..(312837)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (312993)..(312993)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (319226)..(319226)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559167)..(559167)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559241)..(559241)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (600992)..(600992)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (622708)..(622708)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (657081)..(657081)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (657203)..(657203)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (674435)..(674435)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (682442)..(682442)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (713652)..(713652)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (741684)..(741684)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (779455)..(779455)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (779676)..(779676)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (855539)..(855539)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature

LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1349491)..(1349491)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1470091)..(1470091)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1569020)..(1569020)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1664854)..(1664854)
OTHER INFORMATION: n equals a, t, c, or g

S-08-916-421B-1

Query Match 6.8%; Score 34; DB 4; Length 1664976;
Best Local Similarity 50.6%; Pred. No. 34;
Matches 82; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
y 272 GAATCATTAGACTCAGGATTCATCGTTAGTCATTTAGACGATGAATCTGAAGCACAG 331
b 75057 GAAGTTGAAAATACTGCCATTAGTTTAAATGAAGATGATGCCAGCAGTTGTTGAAAAA 74998
y 332 CTTCCAGAAATTTTACACACATTTGTACAAAACCTGGAGGTTTCTCTTAAAAAATTA 391
b 74997 AATTAGATGATTTTGGAGAAGTATCAACAAGCTTCAATACTTAGGCTTTAAAAAAGTT 74938
y 392 GATGCATCTATCAACATCGCTTATTAATAATATTTAT 433
b 74937 GAACCTCTTTACATCAGATATGTTAAAGATTTAATAT 74896

earch completed: May 26, 2004, 22:17:38
ob time : 64.2249 secs

137 AGAATCACCACCTGTTTTCATGGCTTAAGATGGTTTGGAAAAATCTTTATATACATTTT 196
Db |||||
61 AGAATCACCACCTGTTTTCATGGCTTAAGATGGTTTGGAAAAATCTTTATATACATTTT 120
QY |||||
197 TCAGAGGATTTGACCTTTATTTGATGAGATGCCATTTATCCCGAAGCTATCTAGAGGAA 256
Db |||||
121 TCAGAGGATTTGACCTTTATTTGATGAGATGCCATTTATCCCGAAGCTATCTAGAGGAA 180
QY |||||
257 GGTACAGATGTTGGAACTCATTAGACTCAGGATTCATCGTTAGTCATTTTAGACGAT 316
Db |||||
181 GGTACAGATGTTGGAACTCATTAGACTCAGGATTCATCGTTAGTCATTTTAGACGAT 240
QY |||||
317 GAATCTGAAGCAGCTTCCAGAAATTTTAGCAGACATTTGACAAAACTTTGGAGGGTTT 376
Db |||||
241 GAATCTGAAGCAGCTTCCAGAAATTTTAGCAGACATTTGACAAAACTTTGGAGGGTTT 300
QY |||||
377 GTCCCTTAAAAAATAGATGTCATCTATACAACTCCGCTTATTAATAATATATTCAATCA 436
Db |||||
301 GTCCCTTAAAAAATAGATGTCATCTATACAACTCCGCTTATTAATAATATATTCAATCA 360
QY |||||
437 CCATTACCAAGTCTGTTTTGAGATAATGGAGAGATGCCATTCGAGAAATTTGTGTAAT 496
Db |||||
361 CCATTACCAAGTCTGTTTTGAGATAATGGAGAGATGCCATTCGAGAAATTTGTGTAAT 420
QY |||||
497 CAAA 500
Db |||||
421 CAAA 424

RESULT 2

US-10-172-118-1480
; Sequence 1480, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1480
; LENGTH: 11490
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_014363
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1480

Query Match 84.8%; Score 424; DB 13; Length 11490;
Best Local Similarity 100.0%; Pred. No. 3.8e-101; Indels 0; Gaps 0;
Matches 424; Conservative 0; Mismatches 0;
QY 77 ATGAATACATTTCTGGCTGSCAGAGAAATTTGATTTCAATGGTATCCATTTGATGAAAC 136
Db 1 ATGAATACATTTCTGGCTGSCAGAGAAATTTGATTTCAATGGTATCCATTTGATGAAAC 60
QY 137 AGAATCACCACCTGTTTTCATGGCTTAAGATGGTTTGGAAAAATCTTTATATACATTTT 196
Db 61 AGAATCACCACCTGTTTTCATGGCTTAAGATGGTTTGGAAAAATCTTTATATACATTTT 120
QY 197 TCAGAGGATTTGACCTTTATTTGATGAGATGCCATTTATCCCGAAGCTATCTAGAGGAA 256

121 TCAGAGGATTTGACCTTTATTTGATGAGATCCCACTTATCCCGAAGCTATCTAGAGGAA 180
QY |||||
257 GGTACAGACATGTTGGAACTCATTAGACTCAGGATTCATCGTTAGTCATTTTAGACGAT 316
Db |||||
181 GGTACAGACATGTTGGAACTCATTAGACTCAGGATTCATCGTTAGTCATTTTAGACGAT 240
QY |||||
317 GAATCTGAAGCAGCTTCCAGAAATTTTAGCAGACATTTGACAAAACTTTGGAGGGTTT 376
Db |||||
241 GAATCTGAAGCAGCTTCCAGAAATTTTAGCAGACATTTGACAAAACTTTGGAGGGTTT 300
QY |||||
377 GTCCCTTAAAAAATAGATGTCATCTATACAACTCCGCTTATTAATAATATATTCAATCA 436
Db |||||
301 GTCCCTTAAAAAATAGATGTCATCTATACAACTCCGCTTATTAATAATATATTCAATCA 360
QY |||||
437 CCATTACCAAGTCTGTTTTGAGATAATGGAGAGATGCCATTCGAGAAATTTGTGTAAT 496
Db |||||
361 CCATTACCAAGTCTGTTTTGAGATAATGGAGAGATGCCATTCGAGAAATTTGTGTAAT 420
QY |||||
497 CAAA 500
Db |||||
421 CAAA 424

RESULT 3

US-10-027-632-245140/c
; Sequence 245140, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 245140
; LENGTH: 1048
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-245140

Query Match 8.0%; Score 40; DB 13; Length 1048;
Best Local Similarity 52.4%; Pred. No. 3.6;
Matches 88; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
QY 104 TTGATTGTTCAATGGTATCCCAATTTGATGAAACAGAAATCACCATCTCTGTTTCATGGCTT 163
Db 924 TTGATATAGAAGCAGTCCTTACAGAAACCCCAATTTTTTTTATCACA 865
QY 164 AGATGGTTTGGAAAAATCTTTATATACATTTTTCAGAGGATTTGACCTTTATTTGATGAG 223
Db 864 AACACAATATTCATCTGTCTCAATATAAACTTTGATAAAGATGTGACATGACAGAGTTG 805
QY 224 ATGCCACTTATCCCGAAGCTATCTAGAGGAGGTCAGACATGTGTG 271
Db 804 AGACACTAGTTCAAGTCATGTCCCGACATCTCTTCAGAAATTTATG 757

APPLICANT: EPIGENOMICS AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC

OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FEATURE:
NAME/KEY: unsure
LOCATION: (379615)
US-10-312-841-2

Query Match 7.7%; Score 38.4; DB 15; Length 3673778;
Best Local Similarity 47.9%; Pred. No. 5.1e+02;
Matches 140; Conservative 0; Mismatches 151; Indels 1; Gaps 1;
QY 172 TTGGAAAAATCTTTATATACATTTTTCAGAGGATTTGACCTTTTATTTGATGAGATGCCACT 231
DB 845551 TTTTATAACCTTAAATAATATCTTTATACATTTCTAATTTTCARAAAATCCCT 845492
QY 232 TATCCCGAGACTACTACT-AGAGGAGGTGAGCATGTGTGGAACTCATTTAGACTCAGA 290
DB 845491 CATCACCATAATTAATCTCCTCTTAAATAACACAAATTTAGTTTATTTACGTAAAC 845432
QY 291 TTCCATCGTTAGTCATTTTATAGCATGATCTGAGCAGCTTCCAGATTTTTCAGCAG 350
DB 845431 ATCCATTAATCTTCTTCTTATCTTATTAATAAATTAACCTTTAATCTTCTTCTTAA 845372
QY 351 ACATTTGTAACAAAATCTGGAGGTTTGTCTTAAATAATTAGATGCACTATACACATC 410
DB 845371 TCACCACATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 845312
QY 411 CGTTTATTAATAATAATATCTTATCAATCAATCAATCAATCAATCAATCAATCAATCA 462
DB 845311 AATATACATAATCAATTAATAATAATAATAATAATAATAATAATAATAATAATAAT 845260

RESULT 8
US-09-969-373-349/c
Sequence 349, Application US/09969373
Patent No. US20020133852A1
GENERAL INFORMATION:
APPLICANT: Haug, Brian M.
APPLICANT: Effertz, Roger J.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 349
LENGTH: 312
TYPE: DNA
ORGANISM: Glycine max
US-09-969-373-349

Query Match 7.6%; Score 37.8; DB 9; Length 312;
Best Local Similarity 48.4%; Pred. No. 7.3; Mismatches 112; Indels 0; Gaps 0;
Matches 105; Conservative 0
QY 178 AATCTTTTATATACATTTTTCAGAGGATTTGACTTTTATTTGATGAGATGCCACTTATCCC 237
DB 297 AATATGTAATAATATATTAGATTAATTTAGAAATAATAATATGATGCTAATGATAAA 238
QY 238 CAGAACTACTAGAGGAGGTGAGCATGTGTGGAACTCATTTAGACTCAGGATTCATC 297
DB 237 ATATAATTTTATATCACTATAAATTTATTTTATTTATAGTTTATTTATTTATTTCCATC 178
QY 298 GTTAGTCATTTTATAGCATGATCTGAGCAGCTTCCAGATTTTTCAGCATTTGT 357
DB 177 ATAAATCAATAATATGATCAATTTTACTGAACTTTTATAATAATAATAATAATAATAAGT 118
QY 358 AAAAAAATCTGGAGGTTTGTCTTAAAAAATAGAT 394

Db 117 ACATTAATGTTGATTTTATTTATTCATCGACATTTGTAAT 81
RESULT 9
US-09-754-853A-4/c
Sequence 4, Application US/09754853A
Publication No. US20030005491A1
GENERAL INFORMATION:
APPLICANT: Haug, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
FILE REFERENCE: 38-10(115810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 4
LENGTH: 513509
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: CDS
LOCATION: (111805)..(113968), (114684)..(115204)
NAME/KEY: unsure
LOCATION: (1)..(513509)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 318013_region_A3
US-09-754-853A-4
Query Match 7.6%; Score 37.8; DB 10; Length 513509;
Best Local Similarity 48.4%; Pred. No. 3.4e+02;
Matches 105; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
QY 178 AATCTTTTATATACATTTTTCAGAGGATTTGACTTTTATTTGATGAGATGCCACTTATCCC 237
DB 477427 AATATGTAATAATATATTAGATTAATTTTAAAGAAAATAAATGATGCTAATGATAAA 477368
QY 238 CAGAACTACTAGAGGAGGTGAGCATGTCAGATGTCGAACTCATTTAGACTCAGGATTCATC 297
DB 477367 ATATTAATTTTATATCACTATATATTTATTTATTTATTTATTTATTTATTTATTTCCATC 477308
QY 298 GTTAGTCATTTTATAGCATGATCTGAGCAGCTTCCAGATTTTTCAGCATTTGT 357
DB 477307 ATAAATCAATAATATGATCAATTTTACTGAACTTTTATAATAATAATAATAATAAGT 477248
QY 358 AAAAAAATCTGGAGGTTTGTCTTAAAAAATAGAT 394
DB 477247 ACATTAATGTTGATTTTATTTATTCGACATTTGTAAT 477211

RESULT 10
US-09-770-149-579/c
Sequence 579, Application US/09770149
Patent No. US20020059663A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Joern
APPLICANT: An, Yong-Giang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Matthew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Woessner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.

APPLICANT: Kricker, Maja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurlan, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 579
LENGTH: 646
TYPE: DNA
ORGANISM: Arabidopsis thaliana
S-09-770-149-579

Query Match 7.5%; Score 37.4; DB 9; Length 646;
Best Local Similarity 48.8%; Pred. No. 14;
Matches 101; Conservative 0; Mismatches 106; Indels 0; Gaps 0;
Y 222 AGATGCCATTATCCCGAGACTATAGAGGAGGTCAGACATGTGTGGAACCTCATTA 281
b 233 AGATCCCCCTTAGCTGAGTGAGTGAATAAGGAGAGATGTGTAAAGAAAAA 174
Y 282 GACTCAGGATTCATCGTTAGTCATTTTAGACGATGAATCTGAACACAGCTTCCAGAT 341
b 173 TGTGTAGGATTTTAGAGTTTTCCTTTCATGTACAAAAAGATGGCTTTACGCCAAT 114
Y 342 TTTTAGACGATGTACAAAAACCTTGGAGGTTTGTCTTAAAAAATAGATGATCTA 401
b 113 GTGTAGATGCTTTTGTAGAACATCCAGCTTTATTTCAGTAAAAAATAAAAAA 54
Y 402 TACAACATCGCTTATTAAAAAATA 428
b 53 AAAAAAATAAAAAAATAAAAAA 27

RESULT 11
S-10-282-122A-18133/c
Sequence 18133, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18133
LENGTH: 1227
TYPE: DNA
ORGANISM: Campylobacter jejuni
US-10-282-122A-18133

Query Match 7.5%; Score 37.4; DB 13; Length 1227;
Best Local Similarity 44.6%; Pred. No. 19;
Matches 146; Conservative 0; Mismatches 181; Indels 0; Gaps 0;
QY 146 CCATCTGTTTCATGCTTAAGATGGTTTGGAAAAATCTTTATATACATTTTCAGAGAT 205
Db 1021 CCAATTCITTTAGCAAAATGATAAATTATTGGCAAAATGACGATTTGGATTGTTTATAAAT 962
QY 206 TTGACTTTTATTTGATGAGTGCCTTATCCCGAAGTACTATAGAGGAGGTCAGACA 265
Db 961 ATACAAATTAATTTGATGAGGAGTAAAGATGACAAATATCAAAAAATTTATAGAC 902
QY 266 TGTGTGGAACTCATTTAGACTCAGGATTCATCGTTAGTCAATTTTAGACGATGAATCTGAA 325
Db 901 ATTCTATAAGATTTTATACCTTAATCGAAAACTAGTAATCTCACCTATACATTTTGA 842
QY 326 GCACACTTCCAGAAATTTTAGCAGACATTTGACAAAACTTGGAGGTTTGTCTTAAA 385
Db 841 TTAAGTTTATAGCAAGGAGTGCACAAATTAACAAAAAGGCAAAAAATCATCTAAA 782
QY 386 AAATTAGATGCATCTATACACATCCGCTTATTAAAAAATATATTTCATTCACCATTAACA 445
Db 781 AAAGTTTGTCTTAAAGAACACAAACAAATACAAATGTTACGCTCATTTAAAACC 722
QY 446 AGTGTGTTTTCAGATTAATGGAGAAG 472
Db 721 ATAATAAATTTTATATATTTTGAAGAAG 695

RESULT 12
US-10-311-455-2026/c
Sequence 2026, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 2026
LENGTH: 11172
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-2026

Query Match 7.5%; Score 37.4; DB 15; Length 11172;
Best Local Similarity 53.8%; Pred. No. 60;
Matches 77; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 299 TTAGTCATTTTACAGCATGAATCTGAAGCACAGCTCCAGAAATTTTACGACAGATTGTA 358
Db 9356 TAAATCACCTTAATCATATAAATCTATAATCCATTTTAAATATTTTATAAAATATAA 9297
QY 359 CAAAAACTGGAGGGTTCTCTTAAAAATAGATGATCATACACATCCCGCTTATT 418
Db 9296 AATTACGTTAAATTTATTTTATCTTTTAAATATCCAAATTTTCAATAACTATTATT 9237
QY 419 AAAAAATATATTCATCCACATT 441
Db 9236 AAAAAAATATCTTTCATATT 9214

RESULT 13
US-10-027-632-117466/c
; Sequence 117466, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 117466
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1140)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-117466

Query Match 7.4%; Score 37.2; DB 13; Length 1140;
Best Local Similarity 49.0%; Pred. No. 21;
Matches 96; Conservative 1; Mismatches 99; Indels 0; Gaps 0;
QY 2 TGATTTACAGGAAGACCATGATCTAGCTGCAGCTTCTTAAATCCAGACGATTTCACGT 61
Db 616 TGTTTAGTTGAATAACATAAAATATTTAAAGTCTCTAATAGTTTCATTGTAAGAAAGG 557
QY 62 CTTATCAGGAAGTAATGAATACATTTCTGGCTGGCAGAGATTGATTTCAATGGTAT 121
Db 556 CTAATGAGATTGTTGAGAAATTTAGGACATAGTACACACTGAATGTAGATGCTRT 497
QY 122 CCATTTGATGAACAGAAATCCACCATCTGTTTCATGGCTTAAGATGTTTGGAAAAAT 181
Db 496 AAACATAAGCCAGCAAGAACGACATTTATTAGATGTTAGTGTCTACTTCGGGAGGAT 437

QY 182 CTTTATATACATTTT 197
Db 436 TTTTGTCTTCTATATT 421
RESULT 14
US-10-027-632-117467/c
; Sequence 117467, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 117467
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1140)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-117467

Query Match 7.4%; Score 37.2; DB 13; Length 1140;
Best Local Similarity 49.0%; Pred. No. 21;
Matches 96; Conservative 1; Mismatches 99; Indels 0; Gaps 0;
QY 2 TGATTTACAGGAAGACCATGATCTAGCTGCAGCTTCTTAAATCCAGACGATTTCACGT 61
Db 616 TGTTTAGTTGAATAACATAAAATATTTAAAGTCTCTAATAGTTTCATTGTAAGAAAGG 557
QY 62 CTTATCAGGAAGTAATGAATACATTTCTGGCTGGCAGAGATTGATTTCAATGGTAT 121
Db 556 CTAATGAGAAATTTGTTGAGAAATTTAGGACATAGTACACACTGAATGTAGATGCTRT 497
QY 122 CCATTTGATGAACAGAAATCCACCATCTGTTTCATGGCTTAAGATGTTTGGAAAAAT 181
Db 496 AAACATAAGCCAGCAAGAACGACATTTATTAGATGTTAGTGTCTACTTCGGGAGGAT 437
QY 182 CTTTATATACATTTT 197
Db 436 TTTTGTCTTCTATATT 421

RESULT 15
US-10-027-632-117466/c
; Sequence 117466, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 32520
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 117466
LENGTH: 1140
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(1140)
OTHER INFORMATION: n = A,T,C or G
S-10-027-632-117466

Query Match 7.4%; Score 37.2; DB 16; Length 1140;
Best Local Similarity 49.0%; Pred. No. 21;
Matches 96; Conservative 1; Mismatches 99; Indels 0; Gaps 0;
y 2 TGATTTACAGGAAGACCAGTGTACTCAGCTGCAGCTTCTAAATCCAGAACGATTTGCACGT 61
b 616 TGTGTTAGTTGAATAACATAAAATATTTAAAGTCTCTAATAGTTCAATTTGAAAAGGAGG 557
y 62 CTTATCAAGGAGTATGATACATCTCGCCTGGCAGAGATTTGATTTCAATGGTAT 121
b 556 CTAATGAGAAATTTTCAGAAATTTAGGACATAGTACACACTGAATGTAGATGCTRT 497
y 122 CCATTTGATGAAACAGAAATCACCACATCTGTTTCATGCTTTAAGATGGTTGGAAAAAT 181
b 496 AACATAAGCCAGCAGAGAAAGCACTTATTAGATGGTAGTCTGCTACTTCGGAGGAT 437
y 182 CTTTATATACATTTT 197
b 436 TTTTGTCTCTATATT 421

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ob time : 374.131 secs

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M nucleic - nucleic search, using sw model

run on: May 26, 2004, 20:25:31 ; Search time 45.0924 Seconds
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effect score: 401
sequence: 1 gtacagtaaaactaggagc.....actggacagtggatagg 401

scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

searched: 682709 seqs, 277475446 residues

total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*

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- 2: /cgn2_6/prodata/2/ina/5B COMB.seq.*
- 3: /cgn2_6/prodata/2/ina/6A COMB.seq.*
- 4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
- 5: /cgn2_6/prodata/2/ina/PCUS COMB.seq.*
- 6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	42.6	10.6	7218	1	Sequence 14, Appl
C 2	34.8	8.7	1607	4	Sequence 296, App
C 3	34.2	8.5	981	4	Sequence 2087, Ap
C 4	33.8	8.4	5385	4	Sequence 1, Appli
C 5	33.8	8.4	83450	4	Sequence 3, Appli
C 6	33.4	8.3	1365	4	Sequence 2333, Ap
C 7	33.4	8.3	1664976	4	Sequence 1, Appli
C 8	33	8.2	1830121	4	Sequence 1, Appli
C 9	33	8.2	1830121	4	Sequence 1, Appli
C 10	32.8	8.2	92407	4	Sequence 36, Appl
C 11	32.8	8.2	580073	4	Sequence 1, Appli
C 12	32.4	8.1	1335	4	Sequence 7, Appli
C 13	32.4	8.1	1425	4	Sequence 339, App
C 14	32.4	8.1	1651	4	Sequence 598, App
C 15	32.2	8.0	4138	4	Sequence 3, Appli
C 16	32.2	8.0	5807	4	Sequence 245, App
C 17	31.8	7.9	360	4	Sequence 137, App
C 18	31.8	7.9	1082	4	Sequence 591, App
C 19	31.8	7.9	2304	1	Sequence 1, Appli
C 20	31.8	7.9	2304	1	Sequence 1, Appli
C 21	31.4	7.8	2718	4	Sequence 14, Appli
C 22	31.4	7.8	26270	4	Sequence 1, Appli
C 23	31.2	7.8	1332	4	Sequence 1419, Ap
C 24	31.2	7.8	3030	4	Sequence 4115, Ap
C 25	31.2	7.8	3624	4	Sequence 398, App
C 26	31.2	7.8	4617	4	Sequence 1, Appli
C 27	31.2	7.8	5109	4	Sequence 2, Appli

Query Match 10.6%; Score 42.6; DB 1; Length 7218;

ALIGNMENTS

RESULT 1

US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PTZgpt-Fis
; US-08-232-463-14

Sequence 16560, A
Sequence 30, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 131, App
Sequence 1, Appli
Sequence 42, Appl
Sequence 117, App
Sequence 216, App
Sequence 1, Appli
Sequence 39, Appl
Sequence 1745, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 4, Appli


```

; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 296:
US-08-956-171E-296.

Query Match      8.7%; Score 34.8; DB 4; Length 1607;
Best Local Similarity 47.3%; Pred. No. 0.67; Indels 0; Gaps 0;
Matches 105; Conservative 0; Mismatches 117;

123 TAAGAGCATCTTAAATGCATATCCTTCTGAAAAGGAATGTGAAAGAGCTTCCTCAAAA 182
    |||||
548 TATCGGTATTCTGATGCGCAITTTACTTGAAAAGAACAATTCGAAAGATTTATAAATC 607
    |||||
183 TGCCTGATGATGCAAAGCGCACGAAATCTGTTTCTGTTTGATCTCTACAGACATCCAGT 242
    |||||
608 AAACATTGAATATAAACACGCAATTTTCAARGTATGTTTTAACGAAACATGCTCCATCAT 667
    |||||
243 TGATGAAATATTTGATGATAGTAGGGCCCCCATGCAAGGCCGACACTTCTGTGNGTACAA 302
    |||||
668 TGATGATATCTTTTGAAGAATATTATTGACAGCGGTCAACGTCTTAAGAAGATTGTGAACA 727
    |||||
303 CAACCAGCCATTTACAGAAGATGATGTTAGAGGAATTCAGAA 344

728 CACATCAAAATCTTGAAGATGATCAATTTGTACAGATGAAAA 769
    |||||

```

RESULT 3
US-09-134-001C-2097
: Sequence 2097. Application US/09134001C

```

; Sequence 2097, Application US/09134001C
;
; GENERAL INFORMATION:
;
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007

```

TITLE OF INVENTION: EPIDERMIDIS FOR
 FILE REFERENCE: GPC-007
 CURRENT APPLICATION NUMBER: US/09/134,000
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,966
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,775
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674

```

; SEQ ID NO 2097
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2097

```

Quorum Match	a 5%	Score	34.2	DB 4	Length	981
--------------	------	-------	------	------	--------	-----

Query Match 8.5%; Score 34.2; DB 4; Length 981;
Best Local Similarity 71.4%; Pred. No. 0.82;
Matches 45; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Matches 45; Conservative 0; Mismatches 18; Indels 0; Gaps 0

QV 164 TGAAGAGCTTCTTCAAAATGCTGATGCAAGGCCACAGAAATCTGTTTGTCTTG 223

Qy 164 TGAAGAGCTTCTTCAAAATGCTGATGCAAAAGGCCACAGAAATCTGTTCGCTTGG 223

Db 86 TTAAGAGCTCTTAGAAAATGCAATTGATGCAAGCGCAGAAATTAATATTGAAGTTG 145

DB	86	TTAAAGAGCTCTTAGAAAAATGCAATTGAIGCACAAAGCGACAGAAAATTAATAAATGGAGTCTC
Qy	224 ATC 226	

Qy 224 ATC 226
|
Db 146 AAC 148

DD 146 AAC 148

RESULT 4
US-09-920-804-1

US-09-520-804-1
; Sequence 1, Application US/09920804
; Patent No. 6673899

; PATENT NO.: 6675022
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Seino, Susumu; JCR Pharmaceuticals Co., Ltd.
 ;
 ; TITLE OF INVENTION: Sodium Ion-Permeable Chloride/Bicarbonate Exchanger

APPLICANT: DENSO, SUZUKI
; TITLE OF INVENTION: Sodium Ion-Driven Chloride/Bi-Carbonate Exchanger
; FILE REFERENCE: GP44
; CRYSTAL STRUCTURE NUMBER: ITS/08/920 804

FILE NO. 9
CURRENT APPLICATION NUMBER: US/09/920,804
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ. TO NOS. 9

NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 1

LENGTH: 5385
TYPE: DNA
ORGANISM: Mus musculus
S-09-920-804-1

Query Match 8.4%; Score 33.8; DB 4; Length 5385;
Best Local Similarity 50.3%; Pred. No. 2.2;
Matches 83; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

33 ACACAAAGCCTTAGAAGATATGATCCATGCTGCTTTTACACACTGGCAGCAAGATT 92
b 810 ACCAAATTCATGATATAAATGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 869
93 TGGGCGAAGAAAGAAATGACACAGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 152
b 870 TGTGAGATAAAGATGATGTCAGCAGGGAACACACACTAGACTTCAGCAAGTTGA 929
94 153 AAAGGAATGTTGAAGAGCTTTTCAAAATGCTGATGATGCAAA 197
b 930 TCTGCTTTTATGAAAAGATTCCTCGGGTGTCTGAAGCTTCAAA 974

RESULT 5
US-09-811-469-3
Sequence 3, Application US/09811469
Patent No. 6551809
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001171
CURRENT APPLICATION NUMBER: US/09/811,469
CURRENT FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 83450
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(83450)
OTHER INFORMATION: n = A, T, C or G

US-09-811-469-3
Query Match 8.4%; Score 33.8; DB 4; Length 83450;
Best Local Similarity 54.4%; Pred. No. 6.8;
Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

85 ACAGAAATTTGGCGAAGAAAGAAATTCACACAGCAAGTCAAGCAATTAAGCATCTTAATGCATAT 144
b 79171 AAAGAGTCTGAGACAAAGAAAGAAATTAAGTATCAGGATTTAAAGCTTAAGGATATCAATAA 79230
94 145 CTTCTCAAGAGAAATGTTGAAGAGCTTTCTTCAAAATGCTGATGATGCAAGGCGCA 204
b 79231 TCAATTAATGTAATGTTTCCAAACACACCCCATTAAGACAGAGGTTAAGTTGGATTCA 79290
94 205 GAAAT 209
b 79291 AAAGT 79295

RESULT 6
US-09-134-001C-2333
Sequence 2333, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2333
LENGTH: 1365
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2333

Query Match 8.3%; Score 33.4; DB 4; Length 1365;
Best Local Similarity 47.8%; Pred. No. 1.6;
Matches 97; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

123 TAAGAGCATCTTAATGATATCTCTGAAAGGAAATGTTGAAAGAGCTTTCTTCAAAA 182
b 507 TATCGGTATTCGATGCGAGACTTATTAGAAAGGAACATTCGACCGCGACTTAAAGA 566
94 183 TGTGATGATGCAAGGCGACAGAAATCTGTTTGTGTTGATCTCTAGACAGCATCCAGT 242
b 567 AAATATTGAATATAAAACGCATCTTTAAAGGCATGTTTAAACGAACTTGTCCAACATT 626
94 243 TGATAGAAATTTGATGATAAGTGGGCCCATTTGCAAGGCCGACACTTTGTGTGTACAA 302
b 627 CGATGAAATCTTTGACGAAATATTATGCTCCAGGTCAACGTTTAAAGAGACTATGTGACAGA 686
94 303 CAACAGCCCATTTACAGAGATG 325
b 687 CACAGCTAAAATTTTAGACGATG 709

RESULT 7
US-08-916-421B-1/c
Sequence 1, Application US/08916421B
Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
PATENT NO. 6503729
TITLE OF INVENTION: jannaschii
FILE REFERENCE: P275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
FEATURE:
NAME/KEY: misc feature
LOCATION: (28222)-(1664976)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (28257)-(1664976)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (84773)-(1664976)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (84808)-(1664976)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (84812)-(1664976)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (98120)-(1664976)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature

LOCATION: (98159)..(98159)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (98239)..(98239)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (98266)..(98266)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (98343)..(98343)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (103998)..(103998)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (148948)..(148948)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (163385)..(163385)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (191989)..(191989)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (191995)..(191995)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (231980)..(231980)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (234187)..(234187)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (234220)..(234220)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (234814)..(234814)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (309398)..(309398)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (309418)..(309418)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (312837)..(312837)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (312993)..(312993)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (559167)..(559167)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (559241)..(559241)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (600992)..(600992)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (622708)..(622708)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (657081)..(657081)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (657203)..(657203)	OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature	
LOCATION: (674435)..(674435)	OTHER INFORMATION: n equals a, t, c, or g

213 TTTTGTGTTGATCCTAGACAGATCCAGTTGATAGATATTTGATGATTAAGTGGGCCCC 272
761181 TGGATGATGGACCTATGAGTTTCCAAAGGAGATACTCACTGTTATGGGATTGTTA 761122
273 ATTGCAAGGCCAGCACTT 291
761121 CTTTAAAGGACCACCATTT 761103

RESULT 8
US-09-557-884-1/c
Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-557-884-1
Query Match 8.2%; Score 33; DB 4; Length 1830121;
Best Local Similarity 52.6%; Pred. No. 39;
Matches 72; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
Y 166 AAGAGCTTCTTCAAAATGCTGATGCAAGGCGACAGAAATCTGTTTGTGTTGAT 225
Db 1300730 AAGATGTTGTTGATTTACATAACAAGTTGAGAAAAATTCAGTTAATGCTTGA 1300671
Y 226 CCTAGACAGATCCAGTTGATAGATATTTGATGATTAAGTGGGCCCCCATTCGAAGGCCA 285
Db 1300670 ACCAAAGTGACTGCAGTTGAAGCAAAAGATGATGTTATCTACGTTTCAATGGAAGCAA 1300611
Y 286 GCATTTGTGTGTACAA 302
Db 1300610 GCATGTAATGATACCAA 1300594

RESULT 9

US-09-643-990A-1/c
Sequence 1, Application US/09643990A
Patent No. 6528289
GENERAL INFORMATION:
APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186PIC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
TELEFAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-643-990A-1
Query Match 8.2%; Score 33; DB 4; Length 1830121;
Best Local Similarity 52.6%; Pred. No. 39;
Matches 72; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
Y 166 AAGAGCTTCTTCAAAATGCTGATGCAAGGCGACAGAAATCTGTTTGTGTTGAT 225
Db 1300730 AAGATGTTGTTGATTTACATAACAAGTTGAGAAAAATTCAGTTAATGCTTGA 1300671
Y 226 CCTAGACAGATCCAGTTGATAGATATTTGATGATTAAGTGGGCCCCCATTCGAAGGCCA 285
Db 1300670 ACCAAAGTGACTGCAGTTGAAGCAAAAGATGATGTTATCTACGTTTCAATGGAAGCAA 1300611
Y 286 GCATTTGTGTGTACAA 302
Db 1300610 GCATGTAATGATACCAA 1300594

RESULT 10
US-09-596-002-36
Sequence 36, Application US/09596002
Patent No. 6632636
GENERAL INFORMATION:
APPLICANT: Lagace, Robert, E.

APPLICANT: Patterson, Chandra
APPLICANT: Berg, Kim, L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
FILE REFERENCE: PM-0008-4 US
CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PERL Program
SEQ ID NO 36
TYPE: DNA
LENGTH: 92407
ORGANISM: M. catarrhalis
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte template ID No. 6632636 36
PUBLICATION INFORMATION:
US-09-596-002-36

Query Match 8.2%; Score 32.8; DB 4; Length 92407;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 82; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 130 ATCCCTTAATGCATATCCTTCTGAAAGGAAATGTTGAAAGAGCTTCTTCAAAATGCTGAT 189
DB 70322 ATTACTAAGTCATGATTTTAAATAATTTGGTCTACTAGTCCTTTAAATATTAA 70381

QY 190 GATGCAAGGCGACAGAAATCTGTTTGTGTTGATCCTGACAGCATCCAGTTGATAGA 249
DB 70382 ATTGTAAGGCGACCCCAATGCTTTCTTTTAAAGGCGACATGATGATAT 70441

QY 250 ATATTGATGATGAGGCGCCCATTCGACGCGGCGACATTTG 293
DB 70442 CTTTTTCTTACATGATCTTAATTTATCGCTTGATCTG 70485

RESULT 11
US-08-545-528D-1/c
Sequence 1, Application US/08545528D
Patent No. 6537773
GENERAL INFORMATION:
APPLICANT: Fraser et al.
TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment
Patent No. 6537773
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: P8193P1
CURRENT APPLICATION NUMBER: US/08/545,528D
CURRENT FILING DATE: 1995-10-19
PRIOR APPLICATION NUMBER: US 08/488,018
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/473,545
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 580073
TYPE: DNA
ORGANISM: Mycoplasma genitalium
US-08-545-528D-1

Query Match 8.2%; Score 32.8; DB 4; Length 580073;
Best Local Similarity 48.0%; Pred. No. 30;
Matches 94; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 73 ACAACACTTGGCAGCAATTTGGCAGAAAGAAATTCACGAGCAATTAAGAGCATC 132
DB 412879 AAAACACTTTTAAAGAAATAGTACAAAGAACTAATAATATCCTTTTCCACATCTAAA 412820

QY 133 CTTAATGCATATCCTTCTGAAAGGAAATGTTCAAGAGCTTCTTCAAAATGCTGATCAT 192
DB 412819 ATTACTGCTATTCCTCTTGAAGAAATTTATTGGAGAAACATTTTGGTGGTACTGTTGAT 412760

QY 193 GCAAGGCGACAGAAATCTGTTTGTGTTGATCCTAGACAGCATCCAGTTGATAGAATA 252
DB 412759 GAAGCTGAGAAAGAAAGTAATCAATAGTTTCTTTTTTAATGGAATAGATTAAGGTT 412700

QY 253 TTTCATGATAAGTGGG 268
DB 412699 TTAGATAAAATGGG 412684

RESULT 12
US-09-107-532A-7
Sequence 7, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1335
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-107-532A-7

Query Match 8.1%; Score 32.4; DB 4; Length 1335;
Best Local Similarity 52.2%; Pred. No. 3.2;
Matches 72; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 128 GCATCCTTAATGCATATCCTTCTGAAAGGAAATGTTGAAAGAGCTTCTTCAAAATGCTG 187
DB 473 GTATCGTATTGACACTTATTAGATAAAGAAATTTTGAAGACGTTCTTCTGTTGATC 532

QY 188 ATGATCAAGGCGACAGAAATCTGTTTGTGTTTGTATCCTAGACAGCATCCAGTTGATA 247
DB 533 TAGATGACAAAACCGTCATTTGTTGTAATAAATGTTGATTCAGAACCACTTGATTTTGACG 592

248 GAATATTGATGATAGT 265
593 ATATTTTGAAGAATATT 610

Sequence 339, Application US/09134001C
Patent No. 6380370

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GPC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 339
LENGTH: 1425
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-339

Query Match 8.1%; Score 32.4; DB 4; Length 1425;
Best Local Similarity 46.8%; Pred. No. 3.3; Indels 0; Gaps 0;
Matches 102; Conservative 0; Mismatches 116

46 GAAAGATATGATCCCAATGCTGTTTACAACTTGGCAGAGAAATTTGGGCGAGAAAGAA 105
49 GCAGGATATGAGCGCCATCAGAGCTTCTCAATTAGGAAAAAAGTAGCGATAGTAA 108
106 AAATTGACGAGCAGAAATTAAGAGCACTTAAAGCATATCTCTCTGAAAGGAAATGTTG 165
109 AAATCACTCTTAGTGTGACGTGTTACATAAAGGATGATACCTACTAAAGCACTTTTA 168
166 AAAGAGCTTCTCAAAATGCTGATGATGCAAAAGCGCAGAGAAATCTGTTTGTGTTGAT 225
169 AAATCGCTGAGTCAATCATATTAATAAAGCGCATACATTTGGAAATGATGTCAT 228
226 CCTAGACAGATCCAGTTGATAGAAATTTGATGATAA 263
229 CATTTTAAATTAATTTCCCTAAATTTTAGAACGTAA 266

Sequence 598, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny

TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 598
LENGTH: 1651
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 344186.12
US-09-976-594-598

Query Match 8.1%; Score 32.4; DB 4; Length 1651;
Best Local Similarity 60.0%; Pred. No. 3.5; Indels 0; Gaps 0;
Matches 54; Conservative 0; Mismatches 36

15 AGAGCAGTCCCAAGCGACACAAAGCCTTAGAAGATATGATCCATGCTGTTTAC 74
827 AGGAGCTTCTACAGCGCAAAAGAAAGTCTGGAAGTCAATGGATCGCAGAAATCTTTG 886
75 AACACTTGGCAGAGAAATTTGGGCGAGAAAGA 104
887 AAAAATTTGCACAGAAATGTTGGCGAGAAACA 916

Sequence 3, Application US/09920804
Patent No. 6673899
GENERAL INFORMATION:
APPLICANT: Seino, Susumu; JCR Pharmaceuticals Co., Ltd.
TITLE OF INVENTION: Sodium Ion-Driven Chloride/Bi-Carbonate Exchanger
FILE REFERENCE: GP44
CURRENT APPLICATION NUMBER: US/09/920,804
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 3
LENGTH: 4138
TYPE: DNA
ORGANISM: Homo sapiens
US-09-920-804-3

Query Match 8.0%; Score 32.2; DB 4; Length 4138;
Best Local Similarity 49.7%; Pred. No. 5.9; Indels 0; Gaps 0;
Matches 82; Conservative 0; Mismatches 83

33 ACACAAAGCCTTAGAAGATATGCAATCTGTTTACAACTTGGCAGAGAAAT 92
826 ACCAAATTCATGACAAAATGCAAGTCAAGTCTGTTCTCTCAGTCTGCTCCAGCTG 885
93 TGGGCGAAGAAAAATTCACGAGCAATTAAGAGCATCCTTAATGATATCCTTCTGA 152
886 TGTGAAAAATAAAATGATGTTAGCAGAGAAACACAGCACTGTTGACTTTAGCAAGTTGA 945
153 AAAGGAAATGTTCAAGAGCTTCTTCAAAATGCTGATGATGCAA 197
946 TCTGCAATTTATGAAAAAGATTCCTCCAGTGTGAGCATCGAA 990

Search completed: May 26, 2004, 22:17:47
Job time : 54.0924 secs

GenCore version 5.1.1.6
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M nucleic - nucleic search, using sw model

un on: May 26, 2004, 22:02:32 ; Search time 293.637 Seconds

(without alignments)
6206.420 Million cell updates/sec

title: US-09-693-205A-7_COPY_5300_5700

effect score: 401
sequence: 1 Gtagcagtaaaactaggagc.....actggacagtagtggaatagg 401

coreing table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

searched: 2953938 seqs, 2272363821 residues

total number of hits satisfying chosen parameters: 5907676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Match	Length	ID	Description
1	401	100.0	11490	13	US-10-342-887-1480
2	401	100.0	11490	13	Sequence 1480, Ap
3	39.8	9.9	405	13	Sequence 1480, Ap
4	39	9.7	853	13	Sequence 107847,
5	39	9.7	853	13	Sequence 174049,
6	36.6	9.1	954	13	Sequence 174049,
7	36.2	9.0	1116	13	Sequence 16079, A
8	35.8	8.9	54945	10	Sequence 16079, A
9	34.8	8.7	857	16	Sequence 18335, A
10	34.8	8.7	1281	9	Sequence 10, Appl
11	34.8	8.7	1284	9	Sequence 30535, A
12	34.8	8.7	1607	8	Sequence 4620, Ap
13	34.8	8.7	1607	8	Sequence 8577, Ap
14	34.8	8.7	3825	13	Sequence 296, App
					Sequence 236, App
					Sequence 17088, A

Sequence 1702, Ap
Sequence 1, Appli
Sequence 34924, A
Sequence 681, App
Sequence 3, Appli
Sequence 21745, A
Sequence 8371, Ap
Sequence 1851, Ap
Sequence 1, Appli
Sequence 3, Appli
Sequence 199, App
Sequence 199, App
Sequence 199, App
Sequence 199, App
Sequence 263, App
Sequence 18133, A
Sequence 101094,
Sequence 4204, A
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 320, App
Sequence 365, App
Sequence 320, App
Sequence 365, App
Sequence 54592, A
Sequence 54592, A
Sequence 118568,
Sequence 118568,

ALIGNMENTS

RESULT 1

US-10-342-887-1480
; Sequence 1480, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Rudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijter, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1480
; LENGTH: 11490
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1480

Query Match 100.0%; Score 401; DB 13; Length 11490;
Best Local Similarity 100.0%; Pred. No. 5.5e-104;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTAGCAGTAAACTAGCAGCAGTCCCAAGCAGCAGCAGCAGCAGTATGATTC 60
Db 5224 GTAGCAGTAAACTAGCAGCAGTCCCAAGCAGCAGCAGCAGCAGTATGATTC 5283

QY 61 AATGCTCTGTTTACAACTTGGCCACAGAAATTTGGCCAGAGAAATTTGACCCAGCAGA 120
Db 5284 AATGCTCTGTTTACAACTTGGCCACAGAAATTTGGCCAGAGAAATTTGACCCAGCAGA 5343
QY 121 ATTAAGAGCATCCTTTAATGCATATCTTTCTGAAAAGGAAATGTTGAAAGAGCTTCTTCAA 180
Db 5344 ATTAAGAGCATCCTTTAATGCATATCTTTCTGAAAAGGAAATGTTGAAAGAGCTTCTTCAA 5403
QY 181 AATGCTGATGATGCAAGGCGACAGAAATCTGTTTGTGTTGATCTTACAGCAGCATCCA 240
Db 5404 AATGCTGATGATGCAAGGCGACAGAAATCTGTTTGTGTTGATCTTACAGCAGCATCCA 5463
QY 241 GTTGATAGAAATTTGATGATAAGTGGGCCCATTTGCAAGGGCCAGCACATTTGTGTGTAC 300
Db 5464 GTTGATAGAAATTTGATGATAAGTGGGCCCATTTGCAAGGGCCAGCACATTTGTGTGTAC 5523
QY 301 AACACCCAGCCATTTACAGAGATGATGTTAGAGAAATTCAGAAATCTTGGAAAAGGCACG 360
Db 5524 AACACCCAGCCATTTACAGAGATGATGTTAGAGAAATTCAGAAATCTTGGAAAAGGCACG 5583
QY 361 AAAGAGGGAATCCTTATATAAACTGGACAGTATGGAATAGG 401
Db 5584 AAAGAGGGAATCCTTATATAAACTGGACAGTATGGAATAGG 5624

RESULT 2
US-10-172-118-1480
; Sequence 1480, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10172,118
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1480
; LENGTH: 11490
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_014363
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1480

Query Match 100.0%; Score 401; DB 13; Length 11490;
Best Local Similarity 100.0%; Pred. No. 5,5e-104;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAGCAGTAAACTAGGACAGTCCCAAGCGACACAAAGCCTTAGAAAGATATGCAATCC 60
Db 5224 GTAGCAGTAAACTAGGACAGTCCCAAGCGACACAAAGCCTTAGAAAGATATGCAATCC 5283

QY 61 AATGCTGTTTACACACTTGGCCAGAGAAATTTGGCCAGAGAAATTTGACCCAGCAGA 120
Db 5284 AATGCTGTTTACACACTTGGCCAGAGAAATTTGGCCAGAGAAATTTGACCCAGCAGA 5343
QY 121 ATTAAGAGCATCCTTTAATGCATATCTTTCTGAAAAGGAAATGTTGAAAGAGCTTCTTCAA 180
Db 5344 ATTAAGAGCATCCTTTAATGCATATCTTTCTGAAAAGGAAATGTTGAAAGAGCTTCTTCAA 5403
QY 181 AATGCTGATGATGCAAGGCGACAGAAATCTGTTTGTGTTGATCTTACAGCAGCATCCA 240

Db 5404 AATGCTGATGATGCAAGGCGACAGAAATCTGTTTGTGTTGATCTTACAGCAGATCCA 5463
QY 241 GTTGATAGAAATTTGATGATAAGTGGGCCCATTTGCAAGGGCCAGCACATTTGTGTGTAC 300
Db 5464 GTTGATAGAAATTTGATGATAAGTGGGCCCATTTGCAAGGGCCAGCACATTTGTGTGTAC 5523
QY 301 AACACCCAGCCATTTACAGAGATGATGTTAGAGAAATTCAGAAATCTTGGAAAAGGCACG 360
Db 5524 AACACCCAGCCATTTACAGAGATGATGTTAGAGAAATTCAGAAATCTTGGAAAAGGCACG 5583
QY 361 AAAGAGGGAATCCTTATATAAACTGGACAGTATGGAATAGG 401
Db 5584 AAAGAGGGAATCCTTATATAAACTGGACAGTATGGAATAGG 5624

RESULT 3
US-10-424-599-107847
; Sequence 107847, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 107847
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_68401C.1
US-10-424-599-107847

Query Match 9.9%; Score 39.8; DB 13; Length 405;
Best Local Similarity 47.7%; Pred. No. 0.42; 127; Indels 0; Gaps 0;
Matches 116; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 87 AGAATTTGGCGAGAAAGAAATTTGACCCAGCAGAAATTAAGAGCATCTTAAATGCAATACC 146
Db 148 AGAATTTGGCGAGCAGCGTTGATCTGACGCGCGCATCCGCGAGGTTCTGCTCAACTACCC 207
QY 147 TTCTGAAAAGGAAATGTTGAAAGAGCTTCTTCAAATGCTGATGATCAAAGGCGCAGAGA 206
Db 208 GGAGGGAACCCCGTCTCTGAAGGAGCTCTATACAGACGCGCAGCGCCGCCACCCAC 267
QY 207 AATCTGTTTGTGTTTGTATCTTACAGCAGCATCCAGTTGATAGATATTTGATGATAAGTG 266
Db 268 CGTCTCTCTGCTCGACCGCGCTCCACCTGCGGCTCCCTGCTCTCCGACTCCCT 327
QY 267 GCGCCCATTCAGAGGCGCAGCACATTTGTTGTGTACAAACAGCCATTTACAGAGATGA 326
Db 328 CGCGAGTGGCAGGAGCCGCACTGTTGCTTCAACGACGCGCTTTCACCGAGGAGGA 387
QY 327 TGT 329
Db 388 TTT 390

RESULT 4
US-10-027-632-174049
; Sequence 174049, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 174049
LENGTH: 853
TYPE: DNA
ORGANISM: Human
S-10-027-632-174049

Query Match 9.7%; Score 39; DB 13; Length 853;
Best Local Similarity 56.7%; Pred. No. 1;
Matches 72; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

y 37 AAAGCCTTAGAAGATGTCATCCATGCTCTGTTTACAACTGGCAGCAAAATTTGGG 96
b 16 AAATTCACAGAACTGATGCTTACAAATTTGTAACCTAGATAGAACTCAATAA 75
y 97 CAGAAAGAAAATTCACAGCAGCAAGATTAAGAGCATCCCTTAATGCATATCCTTCTGAAAAG 156
b 76 CAGAAACAAAATAACAGAAAATAAAGCTTGGTTCTGATCTTCTAAGCATAATG 135
y 157 GAAATGT 163
b 136 GAACTGT 142

RESULT 5
S-10-027-632-174049
Sequence 174049, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 174049
LENGTH: 853
TYPE: DNA
ORGANISM: Human
S-10-027-632-174049

Query Match 9.1%; Score 36.6; DB 13; Length 954;
Best Local Similarity 47.9%; Pred. No. 5.3;
Matches 105; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

y 73 ACACACTTGGCAGCAAAATTTGGGCGAGAAAGAAATTCACCAGCAGCAATTAAGAGCATC 132

Query Match 9.7%; Score 39; DB 16; Length 853;
Best Local Similarity 56.7%; Pred. No. 1;
Matches 72; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

y 37 AAAGCCTTAGAAGATGTCATCCATGCTCTGTTTACAACTGGCAGCAAAATTTGGG 96
b 16 AAATTCACAGAACTGATGCTTACAAATTTGTAACCTAGATAGAACTCAATAA 75
y 97 CAGAAAGAAAATTCACAGCAGCAAGATTAAGAGCATCCCTTAATGCATATCCTTCTGAAAAG 156
b 76 CAGAAACAAAATAACAGAAAATAAAGCTTGGTTCTGATCTTCTAAGCATAATG 135
y 157 GAAATGT 163
b 136 GAACTGT 142

RESULT 6
US-10-282-122A-16079
Sequence 16079, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITEA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16079
LENGTH: 954
TYPE: DNA
ORGANISM: Clostridium botulinum
US-10-282-122A-16079

Query Match 9.1%; Score 36.6; DB 13; Length 954;
Best Local Similarity 47.9%; Pred. No. 5.3;
Matches 105; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

y 73 ACACACTTGGCAGCAAAATTTGGGCGAGAAAGAAATTCACCAGCAGCAATTAAGAGCATC 132

123 TAAGAGCATCTTAATGATATCTCTTCTGAAAGGAAATGTTGAAAGAGCTTCTTCAAAA 182
 927 TAATAAAACAAATAGAGTAATGCAGAGGAAAGGATATATTGGAAGCGATTTTAAATAC 986
 183 TGCTGATGATGCGAAGCGGACAGAAATCTGTTTGTGTTGATCTCTAGACAGATCCAGT 242
 987 TAGTAATGCACTATATATTACAAATAAGAGACTAGAAAATTTTAAATAGTCTTGAGCAATT 1046
 243 TGATAGAAATATTTGATGATAA 263
 1047 TTATAGGTATTGAAAAATAA 1067

RESULT 8

US-09-967-669-10
 ; Sequence 10, Application US/09967669
 ; Publication No. US20030092650A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Susan M. Freiler
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF SPHINGOSINE-1-PHOSPHATE LYASE EXPRESSION
 ; FILE REFERENCE: RTS-0259
 ; CURRENT APPLICATION NUMBER: US/09/967,669
 ; CURRENT FILING DATE: 2001-09-28
 ; NUMBER OF SEQ ID NOS: 90
 ; SEQ ID NO 10
 ; LENGTH: 54945
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-967-669-10

Query Match 8.9%; Score 35.8; DB 10; Length 54945;
 Best Local Similarity 52.3%; Pred. No. 73;
 Matches 102; Conservative 0; Mismatches 92; Indels 1; Gaps 1;

30 GCGACACAAAGCCCTTAGAAGATATGATCCATCTCTGTTTACAAACACTTGGCAGAGA 89
 2711 GCAAGACCAAGACTTAGAAGAGATGAGATGGTAGATGTTGACGCTCTTATCCGGGA 2770
 90 ATTTGGGCGAAGAAATTTGACAGAGATTTGACAGAGATTTAGAGCATCTTATGATATCTTC 149
 2771 ATGTACAAATATACAGATGACTGGGCTCCACCTCATCTCCCTCCATCTGCGAGGAGGCC 2830
 150 TGAAGAGAAATGTTGAAAGAGCTTCTTCAAAATGCTGATGATGCAAAAGGCGACAGAAAT 209
 2831 TGACATGTGGATTTTGAAG-GCTCTTGGAGATGCTGACTATCCATGCTAGATGGGCAC 2889
 210 CTGTTTGTGTTGA 224
 2890 CTGATGATGTTTAA 2904

RESULT 9

US-10-369-493-30535
 ; Sequence 30535, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 30535
 ; LENGTH: 857
 ; TYPE: DNA

RESULT 7

US-10-282-122A-18335
 ; Sequence 18335, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITEA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 18335
 ; LENGTH: 1116
 ; TYPE: DNA
 ; ORGANISM: Campylobacter jejuni
 US-10-282-122A-18335

Query Match 9.0%; Score 36.2; DB 13; Length 1116;
 Best Local Similarity 48.8%; Pred. No. 7.5;
 Matches 98; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

63 TGCTGTTTACACACTTGGCAGAGATTTGGGAGAGAAAGAAAATTTGACCCAGCAAT 122
 867 TTTATATCTTATATAAATGGAAATTTAGTTGGTCAAGACAGATGCTAGACTGACAT 926

Db 546 TGATGATATCTTTGAAGAAATATTATGACGCGGTCAACGCTTAAAGAAATTTCTGTAACAGA 605
QY 303 CAACCAGCCATTTTACAGAAGATGATGTTAGAGGAATTCAGAA 344
Db 606 CACATCAAAATCTTTAGACGATGCAATTTGTAGCAGATGAAAA 647

RESULT 11
US-09-815-242-8577
; Sequence 8577, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8577
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1284)
US-09-815-242-8577

Query Match 8.7%; Score 34.8; DB 9; Length 1284;
Best Local Similarity 47.3%; Pred. No. 20;
Matches 105; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
QY 123 TAAGAGCATCTTAATGCAATATCTTCTGAAAGGAATGTTGAAAGAGCTTCTTCAAAA 182
Db 426 TATCGGTATTCGTATGGCAGATTTACTTGAAGAAAGAAACATTCGAAGATTTAAATC 485
QY 183 TGTGATGATGCAAGGCGCAGAAATCTGTTTGTGTTTGTATCTCTAGACGATCCAGT 242
Db 486 AACATTTGAATATTAACAGCATATTTCAAAGGTATGTTTAAAGAAACATGTCATCATT 545
QY 243 TGATAGATTTTGTATGATGATGAGTGGGCCCATTCGAGGGCCGACACTTGTGTGACAA 302
Db 546 TGATGATATCTTTGAAGAAATATTATGACGAGGTCAACGCTTAAAGAAATTTGTAACAGA 605
QY 303 CAACCAGCCATTTTACAGAAGATGATGTTAGAGGAATTCAGAA 344
Db 606 CACATCAAAATCTTTAGACGATGCAATTTGTAGCAGATGAAAA 647

RESULT 12

ORGANISM: Caenorhabditis elegans
1-10-369-493-30535
Query Match 8.7%; Score 34.8; DB 16; Length 857;
Best Local Similarity 50.6%; Pred. No. 17;
Matches 84; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
2 TAGCAGTAAACTAGGACAGTCCCAAGCGCACACAAAGCCTTAGAAAGATATGCAATCCA 61
339 TACCAAAATGTTAAGTTAACTGGCACCCCAAAAGATATTTTCAAAGTTTAAATCAT 398
62 ARGCTGTTTACAACTTGGCAGAGATTTGGCAGAAAGAAATTCACGACGAGAA 121
399 ATTATTTTCTCAAAATGAGAAATGTCTGAATAGAGAACATATTTTCAACGTAA 458
122 TTAAGAGATCTTAAATGCATATCTTCTGAAAGGAAATCTTGAA 167
459 CTATGATCTTCTTGATATCTTCTGTTATTCGGCGAACTATATA 504

RESULT 10
3-09-815-242-4620
Sequence 4620, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4620
LENGTH: 1281
TYPE: DNA
ORGANISM: Staphylococcus aureus

Query Match 8.7%; Score 34.8; DB 9; Length 1281;
Best Local Similarity 47.3%; Pred. No. 20;
Matches 105; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
Y 123 TAAGAGCATCTTAATGCAATATCTTCTGAAAGGAATGTTGAAAGAGCTTCTTCAAAA 182
b 426 TATCGGTATTCGTATGGCAGATTTACTTGAAGAAAGAAACATTCGAAGATTTAAATC 485
Y 183 TGTGATGATGCAAGGCGCAGAAATCTGTTTGTGTTTGTATCTCTAGACGATCCAGT 242
b 486 AACATTTGAATATTAACAGCATATTTCAAAGGTATGTTTAAAGAAACATGTCATCATT 545
Y 243 TGATAGATTTTGTATGATGATGAGTGGGCCCATTCGAGGGCCGACACTTGTGTGACAA 302

US-08-781-986A-296
; Sequence 296, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunech
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 296:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-781-986A-296
Query Match 8.7%; Score 34.8; DB 8; Length 1607;
Best Local Similarity 47.3%; Pred. No. 23;
Matches 105; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
QY 123 TAAGAGCATCTTAATGCATATCTTCTGAAAGGAATGTTGAAGAGCTTCTTCAAAA 182
Db 548 TATCGGTATTCGTATGCGAGATTTACTTGAAGAAGAAACATTCGAAGATTTAAATC 607
QY 183 TGCTGATGATGCAAGGCGACAGAAATCTGTTTGTGTTTGTATCTTAGACAGCATCCAGT 242
Db 608 AAACATTGAATATAAACAAGCATATTTCAAAGGTATGTTTAAAGAAACATGTCATCAT 667
QY 243 TGATAGATATTTGATGATGATGATGCGCCCATTTGAGAGGCGCCAGCATTTGTGTGTACAA 302
Db 668 TGATGATATCTTTGAAGATATTTATGACAGAGTCAACGTTTAAAGAAATTTGTAAACAGA 727
QY 303 CAACAGCGCATTTACAGAAGATGATGTTAGAGGAATTCAGAA 344
Db 728 CACATCAAAAATCTTAGACGATGATTTGTAGCAGATGAAA 769

RESULT 13
US-10-329-624-296
; Sequence 296, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunech
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon

US-10-329-624-296
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: 08/956,171
; FILING DATE: October 20, 1997
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB249P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 296:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 296:
; US-10-329-624-296
Query Match 8.7%; Score 34.8; DB 13; Length 1607;
Best Local Similarity 47.3%; Pred. No. 23;
Matches 105; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
QY 123 TAAGAGCATCTTAATGCATATCTTCTGAAAGGAATGTTGAAGAGCTTCTTCAAAA 182
Db 548 TATCGGTATTCGTATGCGAGATTTACTTGAAGAAGAAACATTCGAAGATTTAAATC 607
QY 183 TGCTGATGATGCAAGGCGACAGAAATCTGTTTGTGTTTGTATCTTAGACAGCATCCAGT 242
Db 608 AAACATTGAATATAAACAAGCATATTTCAAAGGTATGTTTAAAGAAACATGTCATCAT 667
QY 243 TGATAGATATTTGATGATGATGATGCGCCCATTTGAGAGGCGCCAGCATTTGTGTGTACAA 302
Db 668 TGATGATATCTTTGAAGATATTTATGACAGAGTCAACGTTTAAAGAAATTTGTAAACAGA 727
QY 303 CAACAGCGCATTTACAGAAGATGATGTTAGAGGAATTCAGAA 344
Db 728 CACATCAAAAATCTTAGACGATGATTTGTAGCAGATGAAA 769

RESULT 14
US-10-282-122A-17088
; Sequence 17088, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel

QY 497 ATATACCTTTATGCAATTA 514
DB 359 AWRACAAATATAATTA 376

RESULT 2

US-07-867-106-2/C
; Sequence 2, Application US/07867106
; Patent No. 5389526

; GENERAL INFORMATION:
; APPLICANT: Slade, Martin B
; APPLICANT: Chang, Andy C M
; APPLICANT: Williams, Keith L
; TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
; NUMBER OF INVENTION: Slime Moulds of the Genus Dictyostelium
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/867,106

; FILING DATE: 19920625
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PJ 7187
; APPLICATION NUMBER: PCT/AU90/00530
; FILING DATE: 02-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Feeney, Joanne Longo
; REGISTRATION NUMBER: 35,134
; REFERENCE/DOCKET NUMBER: RICE-0002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5852 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2378..5038

; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2378..5038
US-07-867-106-2

Query Match 8.1%; Score 47.8; DB 1; Length 5852;
Best Local Similarity 48.4%; Pred. No. 0.025;
Matches 133; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

QY 67 TCTTATACCAAGTGTAGTATATCTCGAACTGCTTGCACAGACACATTTATTA 126
DB 518 TTTTITGGGCAATTTTTCACCTTTTTCACCTTTTTCACCTTTTTCACCTTTT 459
QY 127 CTGTAGAACACTTGCCTTTATGTTGTGTACATATTTCCACAAATGTTATATTTAT 186
DB 458 CTTTITTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 399
QY 187 ATAGTGGTGTGACAGATGCAATCTTTTGTCTTAAGGTGCTGCAGTTAAAAA 245

DB 398 TAATATTATATATATCTTCATGACCCTCATTTTATAAATTTATGTAGTTAATATA 339
QY 247 AACAACCTTTTCTTTTCATATGCGATGCTAGTGGAGTTTTTTTAACTTTAAAAACATCAA 306
DB 338 AAAATTGTGATCTTTTAAATCTATATCTATTTTATAATAATTTTAAAAAGTTATTAACAAAG 279
QY 307 AATTGTAAATCATTTGTGTTATCTAGTAGTTTAT 341
DB 278 AATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 244

RESULT 3

US-08-617-860B-32
; Sequence 32, Application US/08617860B
; Patent No. 6133506
; GENERAL INFORMATION:
; APPLICANT: Tyfner, R., Bautor, J., Bothmann, H., Filsak, E.,
; APPLICANT: Hvrice-Grandpierre, C., Klein, B., Martin, N.,
; APPLICANT: Miller, A., Schulte, W., Voetz, M., Walek, J.,
; APPLICANT: Schell, J.
; TITLE OF INVENTION: Promoters
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steinberg, Raskin & Davidson, P.C.
; STREET: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,860B
; FILING DATE: 01-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/02950
; FILING DATE: 05-SEP-1994
; APPLICATION NUMBER: DE P4329951.2
; FILING DATE: 04-SEP-1993

; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1850 Base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: Double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Cuphea lanceolata
; IMMEDIATE SOURCE:
; LIBRARY: genomic Lambda FIX II
; CLONE: ClTeg1
; FEATURE:
; NAME/KEY: CAAT-Signal
; LOCATION: 1428..1432
; FEATURE:
; NAME/KEY: TATA-Signal
; LOCATION: 1553..1556
; FEATURE:
; NAME/KEY: Transcription start
; LOCATION: 1585
; FEATURE:
; NAME/KEY: Leguminbox
; LOCATION: 1642..1657
; FEATURE:
; NAME/KEY: Startcodon
; LOCATION: 1797..1799
; FEATURE:
; NAME/KEY: CDS

LOCATION: 1797..1850
j-08-617-860B-32
Query Match 7.9%; Score 46.6; DB 3; Length 1850;
Best Local Similarity 44.8%; Pred. No. 0.037; Indels 0; Gaps 0;
Matches 178; Conservative 0; Mismatches 219;
153 TGTGTACATATTTTCCACAAATGTTATATATATAGTGTGTTGACAGGATGCAATC 212
182 TATTGAAATATTTTGAATATTTTAAATATATTTTAAATATTTTAAATATTTTAAATTC 241
213 TTTTGTCTTAAGAGTCTGACGTTTAAATATTTTAAATATTTTAAATATTTTAAATATTTT 272
242 TTTTAAATATTTTAAATATTTTAAATATTTTAAATATTTTAAATATTTTAAATATTTT 301
273 GTAGTGGAGTGTCTTAACTTTTAAATATTTTAAATATTTTAAATATTTTAAATATTTTAA 332
302 AAATATTTTAAATATTTTAAATATTTTAAATATTTTAAATATTTTAAATATTTTAAAT 361
333 GTAGTTTAAATATTTTAAATATTTTAAATATTTTAAATATTTTAAATATTTTAAATATTT 392
362 AAATATTTTAAATATTTTAAATATTTTAAATATTTTAAATATTTTAAATATTTTAAAT 421
393 TGTGTCTGCGCATGCTTCTTAACTTTTAAATATTTTAAATATTTTAAATATTTTAAAT 452
422 TTGGAGATAACCGAGATTTTAAATATTTTAAATATTTTAAATATTTTAAATATTTTAA 481
453 TGATAATTTAGTTTATATAAGTGTACTGCTGTAATGATGCTAAATATTTTAAATATTTT 512
482 GTCCATTTGCGTTAAACCAACGAGTGTCTGTAACGAATGATTAACGATGATCTATGGA 541
513 TAAGGCGTTACAGAACATGTTGAAATTTTAACTTTTAACTTTTAACTTTTAACTTTTAA 549
542 GAAAGTTTAAAGCAACGAGCTATTATTTTAAATTTTAAATTTTAAATTTTAAATTTT 578

RESULT 4

S-08-605-106-4
Sequence 4, Application US/08605106
Patent No. 5910631
GENERAL INFORMATION:
APPLICANT: Topfer, R.
APPLICANT: Martini, N.
APPLICANT: Schell, J.
TITLE OF INVENTION: MEDIUM CHAIN-SPECIFIC THIOESTERS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
STREET: P.O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,106
FILING DATE: 23-SEPT-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/02935
FILING DATE: 01-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 235.001US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-373-6900
TELEFAX: 612-339-3061
TELEX:

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4098 Base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: : DNS (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cuphea lanceolata
IMMEDIATE SOURCE:
LIBRARY: genomic Lambda FIX II
CLONE: Clitegi
FEATURE:
NAME/KEY: CDS
LOCATION: Join(1797..2294, 2658..2791, 2898..3011, 3132
LOCATION: .3303, 3391..3459, 3672..3941)
FEATURE:
NAME/KEY: Startcodon
LOCATION: 1797..1799
FEATURE:
NAME/KEY: exon II
LOCATION: 1787..2294
FEATURE:
NAME/KEY: intron II
LOCATION: 2295..2657
FEATURE:
NAME/KEY: exon III
LOCATION: 2658..2791
FEATURE:
NAME/KEY: intron III
LOCATION: 2792..2897
FEATURE:
NAME/KEY: exon IV
LOCATION: 2898..3011
FEATURE:
NAME/KEY: intron IV
LOCATION: 3012..3131
FEATURE:
NAME/KEY: exon V
LOCATION: 3132..3303
FEATURE:
NAME/KEY: intron V
LOCATION: 3304..3390
FEATURE:
NAME/KEY: exon VI
LOCATION: 3391..3459
FEATURE:
NAME/KEY: intron VI
LOCATION: 3460..3671
FEATURE:
NAME/KEY: exon VII
LOCATION: 3672..3941
FEATURE:
NAME/KEY: Stopcodon
LOCATION: 3942..3944
US-08-605-106-4

Query Match 7.9%; Score 46.6; DB 2; Length 4098;
Best Local Similarity 44.8%; Pred. No. 0.044; Indels 0; Gaps 0;
Matches 178; Conservative 0; Mismatches 219;
QY 153 TGTGTACATATTTTCCACAAATGTTATATATATAGTGTGTTGACAGGATGCAATC 212
Db 182 TATTGAAATATTTTGAATATTTTAAATATTTTAAATATTTTAAATATTTTAAATTC 241
QY 213 TTTTGTCTTAAGAGTCTGACGTTTAAATATTTTAAATATTTTAAATATTTTAAATATTTT 272
Db 242 TTTTAAATATTTTAAATATTTTAAATATTTTAAATATTTTAAATATTTTAAATATTTT 301
QY 273 GTAGTGGAGTGTCTTAACTTTTAAATATTTTAAATATTTTAAATATTTTAAATATTTT 332

QY 235 AGTTAAACAAACAAACCTTTCTTCAATATGGCATGTAGTGGAGTGTCTTTTAACTTT 294
 Db 1385 AATTAAACAAAGTATCAATTTTAAATTAATCAATGATCATATCTTGTGCTTTTCTTTT 1444
 QY 295 AAAACATCAAAATTTGTTAAATCATTTGTTATCTAGTAGTTTATATATATCGGCTTA 354
 Db 1445 AAAAGATAATTAATCTT---TTATTAATTTATATAATTCATATAAGTAAGTAA 1500
 QY 355 TATTTCCCATGATGATCAGAACTGACATTTAATTCATGTTTGTCTCCCATGTTCTT 414
 Db 1501 TAAATCATCTCACTATTTTCAATTTAAATTTAAATTCACCAAGTAATTAATATAAT 1560
 QY 415 TACTTTAACTATTTCTTTTGCAGAAATGTAAGGTAATGATAATAGTTTATATAAGTG 474
 Db 1561 GATTATATCTGTTTATTAAGAGA---TAATTTGATTATGATTATTTTAAAGACAA 1616
 QY 475 TACTGGCTGTAAGTATGCTAATATATCTTTATGCAATTAAGGCTTACAGAACATGTTG 534
 Db 1617 AATCACTTTAGAACTAGCTTCTTCTTAATTTTCAATTAAGGTAATTAAGAAATTTTAT 1676
 QY 535 AAACCTTTTACCTTTTATTTGGGAATAGGAA 566
 Db 1677 TGTCTTCTTTTAAATTTTGTGTAATGAGCAA 1708

RESULT 10
 US-09-543-681A-3626/c
 ; Sequence 3626, Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BROWN
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 ; FILE REFERENCE: 2709.1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543.681A
 ; PRIOR FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 60/128,706
 ; FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344
 ; SEQ ID NO 3626
 ; LENGTH: 237
 ; TYPE: DNA
 ; ORGANISM: Proteus mirabilis
 US-09-543-681A-3626

Query Match 7.5%; Score 44.6; DB 4; Length 237;
 Best Local Similarity 51.2%; Pred. No. 0.071;
 Matches 104; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
 QY 145 TAGTTTGTGTTACATATTTTCCACAAATGTTATATATATATAGTGGTGGACAGG 204
 Db 210 TATTTTCTATTTATATATATGATATTTAAATTTTATTTCTATTTCTATTTTATAGATA 151
 QY 205 ATGCAATCTTTTGTGCTAAAGTGTCTGAGTTAAACCAACCTTTCTTTCTCA 264
 Db 150 ATACTATATTTATATCTACAGGACTGTATATAAACAACAGTGTGATATAGTAT 91
 QY 265 TATGGCATGATGGAGTGTTTTAACTTTTAAACATCAAAATTTGTTAAATCATGTT 324
 Db 90 TTTAGAAAGATAACACAGATGTTTATATGCAAAATATATCAAAATCAATGGAAGCTGG 31
 QY 325 GTTATCTAGTAGTTTAAATAT 347
 Db 30 GCTCATGGTGTAAATAAT 8

RESULT 11
 US-08-487-826B-13/c
 ; Sequence 13, Application US/08487826B
 ; Patent No. 5993827
 ; GENERAL INFORMATION:
 ; APPLICANT: Sim, Kim L.
 ; APPLICANT: Chitnis, Chetan

APPLICANT: Miller, Louis H.
 APPLICANT: Peterson, David S.
 APPLICANT: Su, Xin-zhaun
 APPLICANT: Wellens, Thomas E.
 TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
 TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSES: Knobbe Martens Olson & Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: California
 COUNTRY: US
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,826B
 FILING DATE: 10-SEP-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Israelsen, Ned
 REGISTRATION NUMBER: 29,655
 REFERENCE/DOCKET NUMBER: NIH121.001CF1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19124 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-487-826B-13
 Query Match 7.5%; Score 44.6; DB 2; Length 19124;
 Best Local Similarity 46.0%; Pred. No. 0.18;
 Matches 188; Conservative 0; Mismatches 219; Indels 2; Gaps 1;
 QY 143 TTTATGTTGTGTGTACATATTTTCCACAAATGTTATATATATATAGTGTGTTGAACA 202
 Db 15896 TTTTATTATTAATAATTTTATTTATTTATTTTATTTTATTTTATTTTATTTT 15837
 QY 203 GGATGCAATCTTTTGTGCTAAAGTGTGCGAGTTAAACCAACCTTTCTTTCTTC 262
 Db 15836 ATTTATTTATTTTATTTTAAATAATTTTATTTATTTATTTATTTATTTT 15777
 QY 263 AATATGGCATGTAGTGGAGTTTAACTTTAAACCAATCAAAATCTGTTAAATCAT 322
 Db 15776 AACATTTTAAATTTTATTTTATTTATTTATTTATTTATTTATTTATTTT 15717
 QY 323 GTGTATCTAGTGTATTAATTAATTAATTCGGCTTATTTTCCCATGATGATCAGACTGAC 382
 Db 15716 CTTTCTTTTGTGTTTATGATATATATTTTATTTTATTTTATTTTATTTTCT--T 15659
 QY 383 ATTTAATTCATGTTTGTCTCGCATGCTTTTACCTTTAAACATATTTCTTTGCGAAGT 442
 Db 15658 CTTTGTGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 15599
 QY 443 TAAAGGTAATGATAATAGTTTATATATAGTGTACGGCTGTAAGTGTAAATATAC 502
 Db 15598 TTTTGTATAATCTTTTCTTTTATTTTATTTTATTTTATTTTATTTTATTTT 15539
 QY 503 TTTATGCAATTAAGGCTTACAGACATGTTGAACTTTTCTTTTCTTTT 551
 Db 15538 TTTTATTTTAAATAATTTTCTCTCTTTTCTCTTTTATTTTATTT 15490

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1 nucleic - nucleic search, using sw model

in on: May 26, 2004, 22:02:32 ; Search time 434.232 Seconds
(without alignments)
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file: US-09-693-205A-7_COPY_12200_12792

Effect score: 593
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Scoring table: IDENTITY NUC
Gap 10.0, Gapext 1.0

searched: 2953838 seqs, 2272363821 residues

total number of hits satisfying chosen parameters: 5907676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications NA:*
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 - 2: /cgn2_6/ptodata/1/pubna/PCT_NEW_PUB.seq:*
 - 3: /cgn2_6/ptodata/1/pubna/US05_NEW_PUB.seq:*
 - 4: /cgn2_6/ptodata/1/pubna/US06_PUBCOMB.seq:*
 - 5: /cgn2_6/ptodata/1/pubna/US07_NEW_PUB.seq:*
 - 6: /cgn2_6/ptodata/1/pubna/PCTUS_PUBCOMB.seq:*
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 - 8: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq:*
 - 9: /cgn2_6/ptodata/1/pubna/US09A_PUBCOMB.seq:*
 - 10: /cgn2_6/ptodata/1/pubna/US09B_PUBCOMB.seq:*
 - 11: /cgn2_6/ptodata/1/pubna/US09C_PUBCOMB.seq:*
 - 12: /cgn2_6/ptodata/1/pubna/US09_NEW_PUB.seq:*
 - 13: /cgn2_6/ptodata/1/pubna/US09A_PUBCOMB.seq:*
 - 14: /cgn2_6/ptodata/1/pubna/US10A_PUBCOMB.seq:*
 - 15: /cgn2_6/ptodata/1/pubna/US10B_PUBCOMB.seq:*
 - 16: /cgn2_6/ptodata/1/pubna/US10C_PUBCOMB.seq:*
 - 17: /cgn2_6/ptodata/1/pubna/US10_NEW_PUB.seq:*
 - 18: /cgn2_6/ptodata/1/pubna/US60_NEW_PUB.seq:*
 - 19: /cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	593	100.0	1317	9	US-09-764-846-39
2	593	100.0	1317	15	US-10-091-483-39
3	579.2	97.7	1387	9	US-09-764-846-113
4	579.2	97.7	1387	15	US-10-091-483-113
5	578	97.5	1709	16	US-10-104-047-51
6	277.2	46.7	307	9	US-09-796-692-5699
7	277.2	46.7	307	15	US-10-040-862-5699
8	277.2	46.7	307	16	US-10-057-475B-5699
9	277.2	46.7	307	16	US-10-154-894B-5699
10	56.6	9.5	11651	15	US-10-311-455-2214
11	56.6	9.5	3673778	15	US-10-312-841-2
12	55	9.3	13038	15	US-10-311-455-1247
13	54.8	9.2	15387	15	US-10-311-455-157
14	54.4	9.2	7918	17	US-10-610-351A-15

15	54.4	9.2	13574	15	US-10-311-455-1289	Sequence 1289, Ap
16	54	9.1	3673778	15	US-10-312-841-1	Sequence 1, Appl
17	52.8	8.9	17848	15	US-10-239-676-28	Sequence 28, Appl
18	52.8	8.9	17848	15	US-10-240-453-38	Sequence 38, Appl
19	52.8	8.9	17848	17	US-10-257-166-58	Sequence 58, Appl
20	52.8	8.9	19087	15	US-10-311-455-765	Sequence 765, Appl
21	52.2	8.8	3855	13	US-10-282-122A-40650	Sequence 40650, A
22	51.6	8.7	8237	13	US-10-221-714A-528	Sequence 528, App
23	51.4	8.7	18512	13	US-10-311-455-949	Sequence 949, App
24	51.2	8.6	5487	15	US-10-311-455-1571	Sequence 1571, Ap
25	51	8.6	9652	15	US-10-311-455-881	Sequence 881, App
26	51	8.6	11805	15	US-10-311-455-1721	Sequence 1721, Ap
27	50.8	8.6	15872	13	US-10-221-714A-241	Sequence 241, App
28	50.6	8.5	4503	15	US-10-311-455-744	Sequence 744, App
29	50.6	8.5	8169	13	US-10-221-714A-9	Sequence 9, Appl
30	50.4	8.5	6294	15	US-10-311-455-1027	Sequence 1027, Ap
31	50.2	8.5	5424	15	US-10-311-455-827	Sequence 827, App
32	50.2	8.5	6038	15	US-10-311-455-38	Sequence 38, Appl
33	50.2	8.5	6101	13	US-10-221-613-10	Sequence 10, Appl
34	50	8.4	50	16	US-10-131-827-768	Sequence 768, Appl
35	50	8.4	50	15	US-10-131-827-7949	Sequence 7949, Ap
36	50	8.4	17419	15	US-10-239-676-100	Sequence 100, App
37	50	8.4	17419	15	US-10-311-455-1288	Sequence 1268, Ap
38	50	8.4	17419	15	US-10-240-453-112	Sequence 112, App
39	50	8.4	20486	15	US-10-240-485-164	Sequence 164, App
40	49.8	8.4	6112	15	US-10-311-455-462	Sequence 462, App
41	49.8	8.4	8423	15	US-10-311-455-1380	Sequence 1380, Ap
42	49.6	8.4	5557	15	US-10-311-455-1519	Sequence 1519, Ap
43	48.8	8.2	5888	15	US-10-240-485-10	Sequence 10, Appl
44	48.6	8.2	6109	13	US-10-221-613-33	Sequence 33, Appl
45	48.6	8.2	6109	15	US-10-311-455-299	Sequence 299, App

ALIGNMENTS

RESULT 1
US-09-764-846-39
; Sequence 39, Application US/09764846
; Patent No. US20020102638A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ12
; CURRENT APPLICATION NUMBER: US/09/764,846
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 1317
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-846-39

Query Match	100.0%;	Score 593;	DB 9;	Length 1317;
Best Local Similarity	100.0%;	Pred. No. 4e-115;		
Matches 593;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ACATCTTATGTTTACAGGCTTCCTCTTTGATGAAGATAGCAACGGAACCTCAAAATGGT	60	
Db	629	ACATCTTATGTTTACAGGCTTCCTCTTTGATGAAGATAGCAACGGAACCTCAAAATGGT	688	
QY	61	GGCAGTCTTATACCACTGTTAGTATGTTTCGGAACCTGTTGCCAAGACACATT	120	
Db	689	GGCAGTCTTATACCACTGTTAGTATGTTTCGGAACCTGTTGCCAAGACACATT	748	
QY	121	TATTAACCTGTAGAACACCTGCTTTATGTTTGTTGTCATATTTTCCAAATGTTATA	180	
Db	749	TATTAACCTGTAGAACACCTGCTTTATGTTTGTTGTCATATTTTCCAAATGTTATA	808	
QY	181	ATTATATAGTGTGGTTGAACAGGATGCACTTTTGTGTCTTAAGGTGTCGAGTTAA	240	

Db 809 ATTTATATAGTGTGTTGAAACAGGATGCAATCTTTTGTGTCTAAAGGTGCTGCAGTTAA 868
Qy 241 AAAAAAACAACCTTTCTTTCAATATGCGCATGTAGTGGAGTTTCTTTTAACTTTTAAAAAC 300
Db 869 AAAAAAACAACCTTTCTTTCAATATGCGCATGTAGTGGAGTTTCTTTTAACTTTTAAAAAC 928
Qy 301 ATCAAAAATTTGTTAAATCAATTTGTTTATCTAGTGTATTAATATCGGCTTATATTTTC 360
Db 929 ATCAAAAATTTGTTAAATCAATTTGTTTATCTAGTGTATTAATATCGGCTTATATTTTC 988
Qy 361 CCCATGAATGATCAGAACTGACATTTAATTCATGTTTGTCTCGCCAGCTTCTTTACTTT 420
Db 989 CCCATGAATGATCAGAACTGACATTTAATTCATGTTTGTCTCGCCAGCTTCTTTACTTT 1048
Qy 421 AACATATTTCTTTTGCAGAACTGAAAGGTAATGATAATTAGTTTATATAGTGTACTGG 480
Db 1049 AACATATTTCTTTTGCAGAACTGAAAGGTAATGATAATTAGTTTATATAGTGTACTGG 1108
Qy 481 CTGTAATGATGCTAAATATATCTTTTATGCAATTAAGGCTTACAGAACATGTTGAAACTT 540
Db 1109 CTGTAATGATGCTAAATATATCTTTTATGCAATTAAGGCTTACAGAACATGTTGAAACTT 1168
Qy 541 TTTTACTTTTATGCGAATAGGAATGTTTGCACCTCCACATTTTATGCTT 593
Db 1169 TTTTACTTTTATGCGAATAGGAATGTTTGCACCTCCACATTTTATGCTT 1221

RESULT 2
US-10-091-483-39
; Sequence 39, Application US/10091483
; Publication No. US20030049650A1
; GENERAL INFORMATION:
; APPLICANT: rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT212C1
; CURRENT APPLICATION NUMBER: US/10/091,483
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 348
; Prior application removed - See File Wrapper or Palm
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 39
; LENGTH: 1317
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-091-483-39

Query Match 100.0%; Score 593; DB 15; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4e-115;
Matches 593; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACATCTTATGTTTACAGGCTTCTGTTGATGAAGATAGCAACGGAAACTCAAAATGGT 60
Db 629 ACATCTTATGTTTACAGGCTTCTGTTGATGAAGATAGCAACGGAAACTCAAAATGGT 688
Qy 61 GGCACTTCTTATPACAGTTGTAGTATGTTTCTGGAACCTGCTTGCACAGACACATT 120
Db 689 GGCACTTCTTATPACAGTTGTAGTATGTTTCTGGAACCTGCTTGCACAGACACATT 748
Qy 121 TATTAACTGTTAGAACACATCTGTTTATGTTGTTGTTATATTTTCCACAAATGTTATA 180
Db 749 TATTAACTGTTAGAACACATCTGTTTATGTTGTTGTTGTTATATTTTCCACAAATGTTATA 808
Qy 181 ATTTATATAGTGTGTTGAAACAGGATGCAATCTTTTGTGTTCTAAAGGTGCTGCAGTTAA 240
Db 809 ATTTATATAGTGTGTTGAAACAGGATGCAATCTTTTGTGTTCTAAAGGTGCTGCAGTTAA 868
Qy 241 AAAAAAACAACCTTTCTTTCAATATGCGCATGTAGTGGAGTTTCTTTTAACTTTTAAAAAC 300
Db 869 AAAAAAACAACCTTTCTTTCAATATGCGCATGTAGTGGAGTTTCTTTTAACTTTTAAAAAC 928
Qy 301 ATCAAAAATTTGTTAAATCAATTTGTTTATCTAGTGTATTAATATCGGCTTATATTTTC 360
Db 929 ATCAAAAATTTGTTAAATCAATTTGTTTATCTAGTGTATTAATATCGGCTTATATTTTC 988

RESULT 3

US-09-764-846-113
; Sequence 113, Application US/09764846
; Patent No. US20020102638A1

; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT212
; CURRENT APPLICATION NUMBER: US/09/764,846
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 113
; LENGTH: 1387
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (23)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (104)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (739)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1378)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1386)
; OTHER INFORMATION: n equals a,t,g, or c

US-09-764-846-113

Query Match 97.7%; Score 579.2; DB 9; Length 1387;

Best Local Similarity 99.3%; Pred. No. 3.3e-112;
Matches 589; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 ACATCTTATGTTTACAGGCTTCTGTTGATGAAGATAGCAACGGAAACTCAAAATGGT 60
Db 620 ACATCTTATGTTTACAGGCTTCTGTTGATGAAGATAGCAACGGAAACTCAAAATGGT 679
Qy 61 GGCAGTCTTATPACAGTTGTAGTATGTTTCTGGAACCTGCTTGCACAGACACATT 120
Db 680 GGCAGTCTTATPACAGTTGTAGTATGTTTCTGGAACCTGCTTGCACAGACACATT 738
Qy 121 TATTAACTGTTAGAACACATCTGTTTATGTTGTTGTTATATTTTCCACAAATGTTATA 180
Db 739 NATTAACCTGTTAGAACACATCTGTTTATGTTGTTGTTATATTTTCCACAAATGTTATA 798
Qy 181 ATTTATATAGTGTGTTGAAACAGGATGCAATCTTTTGTGTTCTAAAGGTGCTGCAGTTAA 240
Db 799 ATTTATATAGTGTGTTGAAACAGGATGCAATCTTTTGTGTTCTAAAGGTGCTGCAGTTAA 858

241 AAAAAAAAAAAGCTTTCTTCAATATGCGATGTAGTGGAGTTTAACTTTAAAAAC 300
859 AAAAAAAAAAAGCTTTCTTCAATATGCGATGTAGTGGAGTTTAACTTTAAAAAC 918
301 ATCAAAATTTGTTAAATCAATTTGTTATCTAGTATGTTTAAATATCGGCTTATATTC 360
919 ATCAAAATTTGTTAAATCAATTTGTTATCTAGTATGTTTAAATATCGGCTTATATTC 978
361 CCCATGAATGATCAGAACCTGACATTTAATTCATGTTCTCGCCATGCTTCTTTACTTT 420
979 CCCATGAATGATCAGAACCTGACATTTAATTCATGTTCTCGCCATGCTTCTTTACTTT 1038
421 AACATATTTCTTTTGCAGAAATGTAAGGTAATGATAATTAAGTTTATATAAGTGTACTGG 480
1039 AACATATTTCTTTTGCAGAAATGTAAGGTAATGATAATTAAGTTTATATAAGTGTACTGG 1098
481 CTGTAATGATGTAATATATCTTTATGCAATTAAGGCTTACAGAACATGTTGAACTT 540
1099 CTGTAATGATGTAATATATCTTTATGCAATTAAGGCTTACAGAACATGTTGAACTT 1158
541 TTTTACTTTTATGGAATAGGAATGTTTGCACCTCCACATTTTATGCTT 593
1159 TTTTACTTTTATGGAATAGGAATGTTTGCACCTCCACATTTTATGCTT 1211

RESULT 4
S-10-091-483-113
Sequence 113, Application US/10091483
Publication No. US20030049650A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: FTZ12C1
CURRENT APPLICATION NUMBER: US/10/091,483
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 348
Prior Application removed - See File Wrapper or Palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 113
LENGTH: 1387
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (23)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc_feature
LOCATION: (104)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc_feature
LOCATION: (739)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc_feature
LOCATION: (1378)
OTHER INFORMATION: n equals a.t.g, or c
NAME/KEY: misc_feature
LOCATION: (1386)
OTHER INFORMATION: n equals a.t.g, or c

98-10-091-483-113
Query Match 97.7%; Score 579.2; DB 15; Length 1387;
Best Local Similarity 99.3%; Pred. No. 3.3e-112;
Matches 589; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
1 ACATCTTATGTTTACAGGCTTCTGTTTATGATGAAGATAGCAACGGAATACTCAAAATGCT 60
620 ACATCTTATGTTTACAGGCTTCTGTTTATGATGAAGATAGCAACGGAATACTCAAAATGCT 679
61 GCCAGTTCTTATTAACAGTTGTTAGTATGTTTCTGGAATGCTTGCACAGCAACATTT 120
680 GCCAGTTCTTATTAACAGTTGTTAGTATGTTTCTGGAATGCTTGCACAGCAACATTT 738
121 TATTAACGTGTAGAACACTGCTTATGTTTGTGTACATATTTTCCAAATGTTTATA 180

Db 739 NATTAACGTGTAGAACACTGCTTATGTTTGTGTACATATTTTCCAAATGTTTATA 798
Qy 181 ATTTATATAGTGTGTTTCAACAGATGCAATCTTTTGTGCTAAAGGTGCTGCAGTTAA 240
Db 799 ATTTATATAGTGTGTTTCAACAGATGCAATCTTTTGTGCTAAAGGTGCTGCAGTTAA 858
Qy 241 AAAAAAACAACCTTTCTTCAATATGCGATGTAGTGGAGTTTAACTTTAAAAAC 300
Db 859 AAAAAAACAACCTTTCTTCAATATGCGATGTAGTGGAGTTTAACTTTAAAAAC 918
Qy 301 ATCAAAATTTGTTAAATCAATTTGTTATCTAGTATGTTTAAATATCGGCTTATATTC 360
Db 919 ATCAAAATTTGTTAAATCAATTTGTTATCTAGTATGTTTAAATATCGGCTTATATTC 978
Qy 361 CCCATGAATGATCAGAACCTGACATTTAATTCATGTTCTCGCCATGCTTCTTTACTTT 420
Db 979 CCCATGAATGATCAGAACCTGACATTTAATTCATGTTCTCGCCATGCTTCTTTACTTT 1038
Qy 421 AACATATTTCTTTTGCAGAAATGTAAGGTAATGATAATTAAGTTTATATAAGTGTACTGG 480
Db 1039 AACATATTTCTTTTGCAGAAATGTAAGGTAATGATAATTAAGTTTATATAAGTGTACTGG 1098
Qy 481 CTGTAATGATGTAATATATCTTTATGCAATTAAGGCTTACAGAACATGTTGAACTT 540
Db 1099 CTGTAATGATGTAATATATCTTTATGCAATTAAGGCTTACAGAACATGTTGAACTT 1158
Qy 541 TTTTACTTTTATGGAATAGGAATGTTTGCACCTCCACATTTTATGCTT 593
Db 1159 TTTTACTTTTATGGAATAGGAATGTTTGCACCTCCACATTTTATGCTT 1211

RESULT 5
US-10-104-047-51
Sequence 51, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392A1el full length cdna
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 51
LENGTH: 1709
TYPE: DNA
ORGANISM: Homo sapiens
US-10-104-047-51

Query Match 97.5%; Score 578; DB 16; Length 1709;
Best Local Similarity 100.0%; Pred. No. 6.4e-112;
Matches 578; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 16 AGGCTTCCTGTTTATGATGAAGATAGCAACGGAATACTCAAAATGTTGCGAGTTCTTATTAC 75
Db 1056 AGGCTTCCTGTTTATGATGAAGATAGCAACGGAATACTCAAAATGTTGCGAGTTCTTATTAC 1115
Qy 76 CAGTTGTAGTATGTTTCTGGAACCTGCTTCCAGACACAACTTTTAACTGTTAGAA 135
Db 1116 CAGTTGTAGTATGTTTCTGGAACCTGCTTCCAGACACAACTTTTAACTGTTAGAA 1175
Qy 136 CACTTGTCTTATCTTTGTGTACATATTTTCCAAATGTTTATATATATAGTGTGG 195
Db 1176 CACTTGTCTTATCTTTGTGTGTACATATTTTCCAAATGTTTATATATATAGTGTGG 1235
Qy 196 TTGAACAGGATGCAATCTTTTGTGCTAAAGGTGCTGCAGTTTAAAAAACAACCTT 255
Db 1236 TTGAACAGGATGCAATCTTTTGTGCTAAAGGTGCTGCAGTTTAAAAAACAACCTT 1295
Qy 256 TTCTTTCAATATGGCATGTAGTGGAGTTTATGTTTAACTTTAAAAAACAATCAAAATGTTTAA 315


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RESULT 14
US-10-610-351A-15
/ Sequence 15, Application US/10610351A
/ Publication No. US20040093632A1
/ GENERAL INFORMATION:
/ APPLICANT: DIXON, RICHARD A.
/ APPLICANT: PAIVA, NANCY L.
/ APPLICANT: XIE, DEYU
/ APPLICANT: SHARMA, SHASHI
/ TITLE OF INVENTION: GENETIC MANIPULATION OF CONDENSED TANNINS
/ FILE REFERENCE: NBLE:004US
/ CURRENT APPLICATION NUMBER: US/10/610,351A
/ CURRENT FILING DATE: 2003-06-30
/ PRIOR APPLICATION NUMBER: 60/392,562
/ PRIOR FILING DATE: 2002-06-28
/ NUMBER OF SEQ ID NOS: 52
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 15
/ LENGTH: 7918
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
US-10-610-351A-15
Query Match          9.2%; Score 54.4; DB 17; Length 7918;

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Best Local Similarity 48.4%; Pred. No. 0.27;
Matches 151; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

QY 86 TATTTGTTCTGGAACCTGCTGCGAAGCAACATTTATTAACTGTTAGAACACACTTGCCTTT 145
Db 4288 TTTAAATTTGTTGTTTTGATAAATAGCTAAAGTTTTTAGCATTTTAAATGAATATTC 4347

QY 146 ATGTTTGTGTTGACATATTTTCCACAAATGTTATATTTATATAGTGTGTTGAACAGGA 205
Db 4348 AAGTTTCCGTTGTTTACATTTTGAAGAAATAAATATTAAATATATTCTGAAGATTTTGT 4407

QY 206 TGCATCTTTTGTGTTGCTAAAGTGTGCTGAGTTTAAAAAACAACCTTTTCTTTCAAT 265
Db 4408 TTTTGTGTTAATCACTACATGACACAGTAAATAGAAAATAATCTATTTTGTGAA 4467

QY 266 ATGCGATGATGAGGAGTTTTTTTAACTTTTAAAAACATCAAAATTTGTTAAATCATTTGT 325
Db 4468 AAGGTATGATCGGTGTTTAGAATACTTTCGAAATCAAAACCGCTATATTCTTAATCA 4527

QY 326 TTATCTAGTAGTTTAAATATATCGGCTTATATTTCCCATGATCATCAGAACTGACATT 385
Db 4528 CTATGTAATATTGTAACCAATTTGGGTTAAACTCAACTAACAACTTCTTAATTAATG 4587

QY 386 TAATTCATGTTT 397
Db 4588 TCATTTTGTTT 4599

RESULT 15
US-10-311-455-1289
; Sequence 1289, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining
; FILE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1289
; LENGTH: 13574
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1289

Query Match 9.2%; Score 54.4; DB 15; Length 13574;
Best Local Similarity 48.0%; Pred. No. 0.34;
Matches 191; Conservative 0; Mismatches 201; Indels 6; Gaps 1;

QY 163 TTTTCCAAATGTTATATATATAGTGTGTTGAACAGGATGCAATCTTTTGTGTC 222
Db 3481 TTTTAGAAAATGTTAGATTTTAAAGTAGTGAAGCGTAAAGTTTTGTTATTTGTAAGTT 3540

QY 223 TAAAGTGTGCTGAGTTTAAAAAACAACCTTTTCTTTCAATATGGCATGTAGTGGAGT 282
Db 3541 GTTTGTTTTTAAATTAATAAATAAATTTAGTTTAAATATAATTTTAAAAAATATTTT 3600

QY 283 TTTTAACTTTTAAACATCAAAATTTGTTAAATCATTTGTTATCTAGTAGTTTATA 342
Db 3601 TGTAGGTTTTTTTAAAGAAAAAATTTTATAAATAATAGTAAGAAATTTAAAGTAATTTTA 3660

QY 343 ATTATCGGCTTATATTTCCCATGATGATCAGAACTGACATTTAATTCATGTTTGTCTC 402

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Db 3661 GTTAGTATAGAAAATAGTTAGATGAATGTCGAAAGAAATTTTATTTGAATATTGTTTG 3720
QY 403 GCCA-----TGCCTCTTTACTTTAAACATATTTCTTTTGCAGAAATGTAAGAGGTAATGAT 456
Db 3721 GTTTGATGTTTGGTATTAAATATTTTATTTTATTTTATATAGTATTTTAGATATAGTTTG 3780
QY 457 AATTAGTTTATATAAGTGTACTGCGCTGTAATGATGCTAAATATATCTTATGCAATTAAAG 516
Db 3781 TTTAAAGTTTATGTTGTGTATATGCTGTATAGATATAAATATTTTGTTTATATAATATTA 3840
QY 517 GCGTTACAGAACATCTTGAACCTTTTCTTTTACTTTTATT 554
Db 3841 TATTTACGTGTGTGATATAAATTTTGGTATTATTTT 3878

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Search completed: May 27, 2004, 01:11:02
Job time : 442.232 secs